FILE

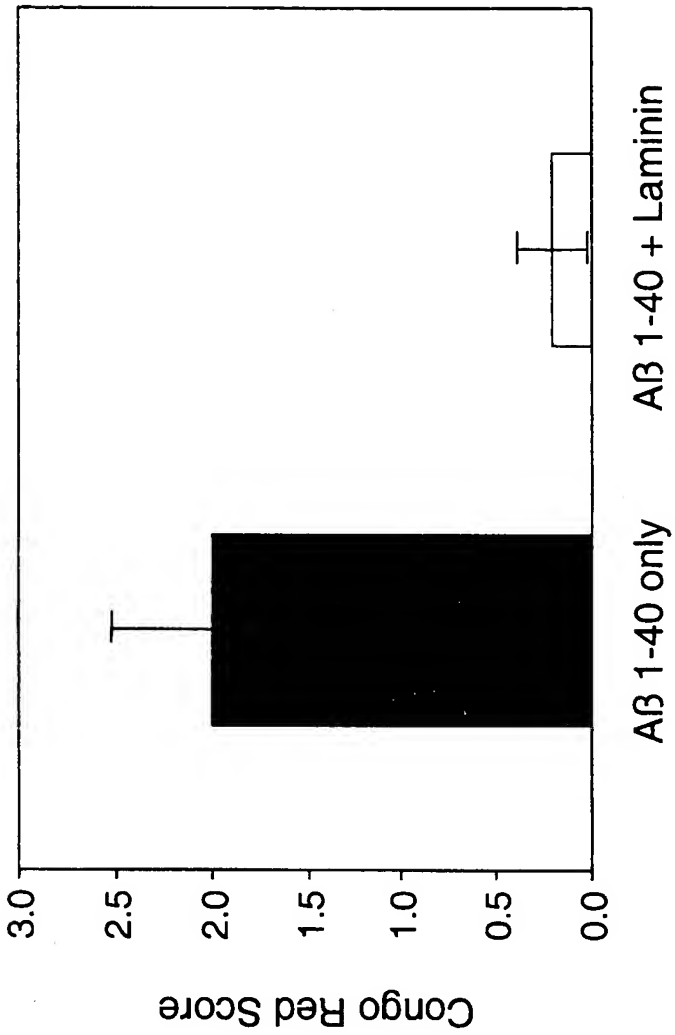


Figure 1

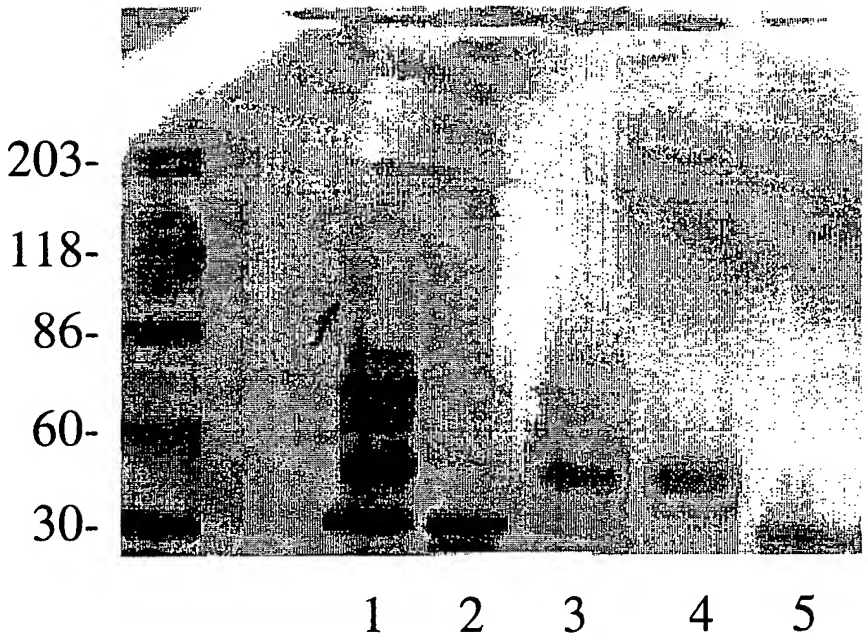


Figure 2

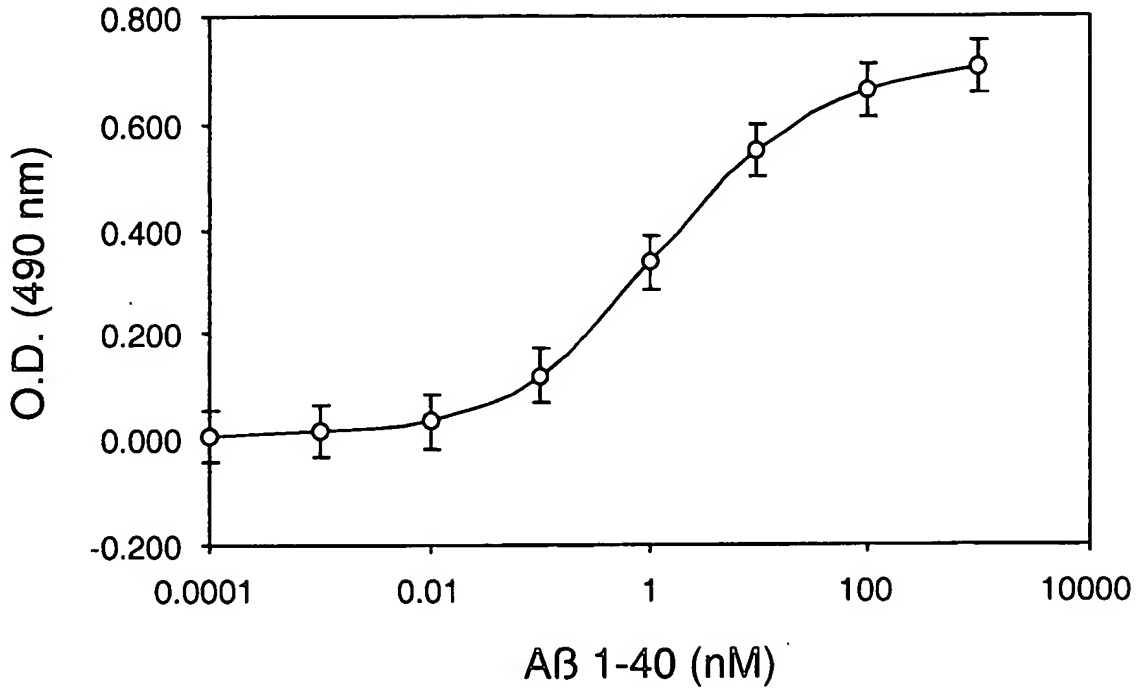

0.800
0.600
0.400
0.200
0.000
-0.200
O.D. (490 nm)
0.0001
0.01
1
100
10000
Aß 1-40 (nM)

Figure 3

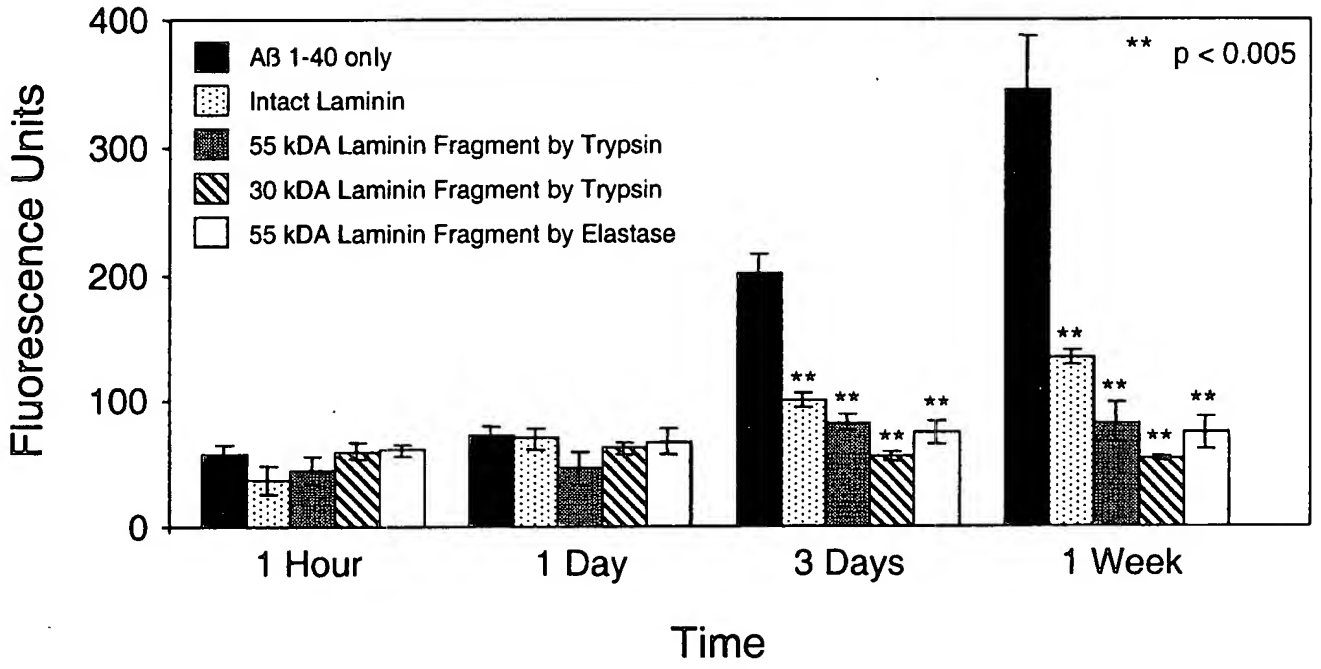

400
300
200
100
0
Fluorescence Units
Aß 1-40 only
Intact Laminin
55 kDA Laminin Fragment by Trypsin
30 kDA Laminin Fragment by Trypsin
55 kDA Laminin Fragment by Elastase
** p < 0.005
1 Hour
1 Day
3 Days
1 Week
Time

Figure 4

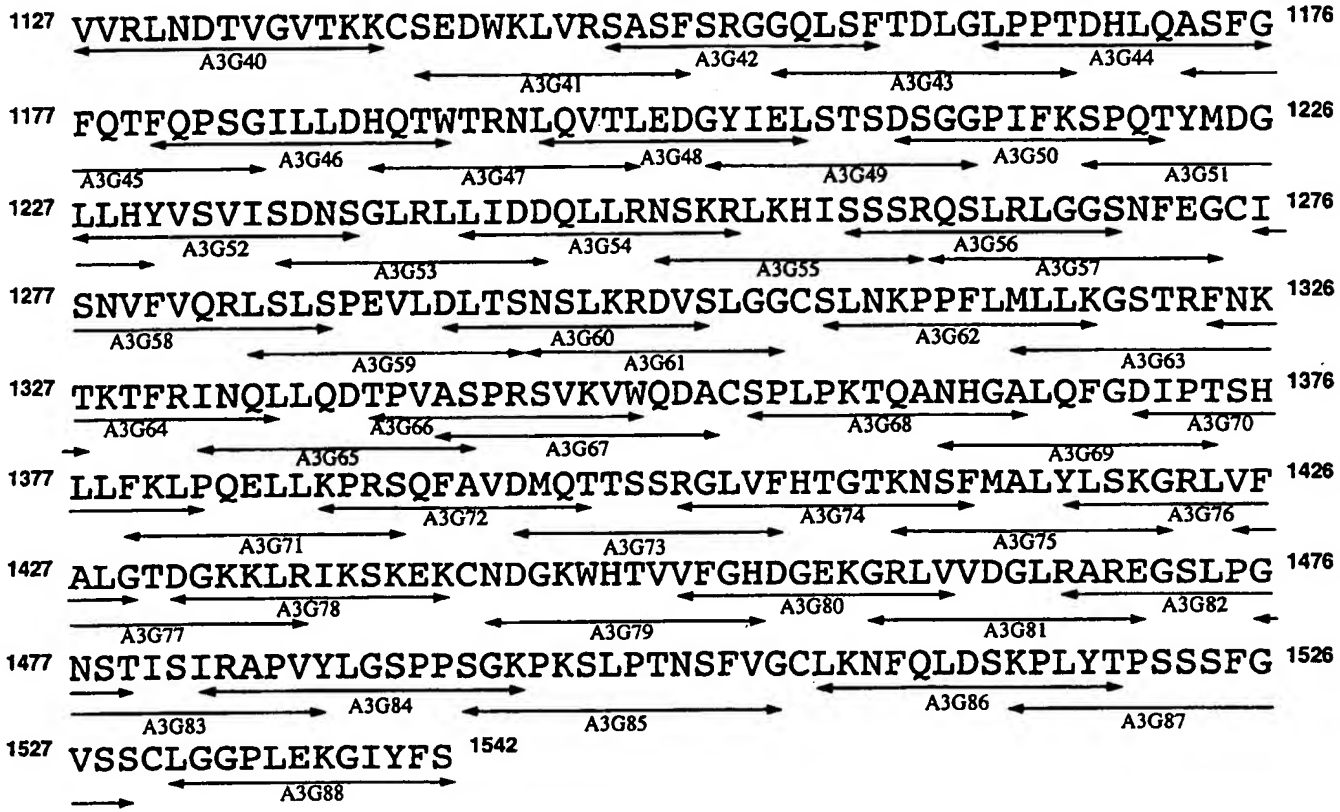

1127 VVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFG 1176
A3G40
A3G41
A3G42
A3G43
A3G44
1177 FQTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDG 1226
A3G45
A3G46
A3G47
A3G48
A3G49
A3G50
A3G51
1227 LLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCI 1276
A3G52
A3G53
A3G54
A3G55
A3G56
A3G57
1277 SNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNK 1326
A3G58
A3G59
A3G60
A3G61
A3G62
A3G63
1327 TKTFRINQLLQDTPVASPRSVKVWQDACSPLPKTQANHGALQFGDIPTSH 1376
A3G64
A3G65
A3G66
A3G67
A3G68
A3G69
A3G70
1377 LLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVF 1426
A3G71
A3G72
A3G73
A3G74
A3G75
A3G76
1427 ALGTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPG 1476
A3G77
A3G78
A3G79
A3G80
A3G81
A3G82
1477 NSTISIRAPVYLGSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFG 1526
A3G83
A3G84
A3G85
A3G86
A3G87
1527 VSSCLGGPLEKGIYFS 1542
A3G88

Figure 5

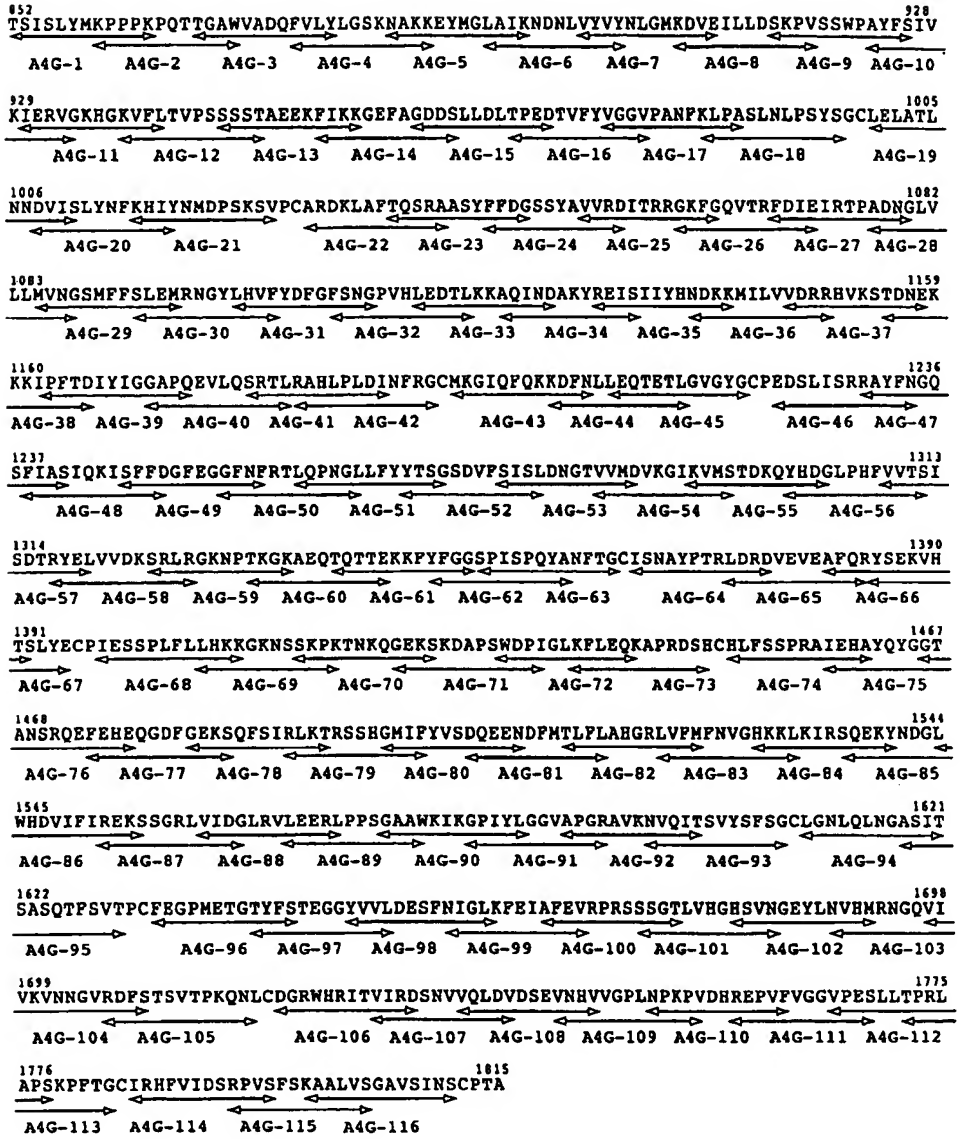

852
TSISLYMKPPPKPQTTGAWVADQFVLYLGSKNAKKEYMGLAIKNDNLVYVYNLGMKDVEILLDSKPVSSWPAYFSIV
928
A4G-1 A4G-2 A4G-3 A4G-4 A4G-5 A4G-6 A4G-7 A4G-8 A4G-9 A4G-10
929
KIERVGKHGKVFLTVPSSSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL
1005
A4G-11 A4G-12 A4G-13 A4G-14 A4G-15 A4G-16 A4G-17 A4G-18 A4G-19
1006
NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQVTRFDIEIRTPADNGLV
1082
A4G-20 A4G-21 A4G-22 A4G-23 A4G-24 A4G-25 A4G-26 A4G-27 A4G-28
1083
LLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVHLEDTLKKAQINDAKYREISIIYHNDKKMILVVDRRHVKSTDNEK
1159
A4G-29 A4G-30 A4G-31 A4G-32 A4G-33 A4G-34 A4G-35 A4G-36 A4G-37
1160
KKIPFTDIYIGGAPQEVLQSRTLRAHLPLDINFRGCMKGIQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFNGQ
1236
A4G-38 A4G-39 A4G-40 A4G-41 A4G-42 A4G-43 A4G-44 A4G-45 A4G-46 A4G-47
1237
SFIASIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVKGIKVMSTDKQYHDGLPHFVVTSI
1313
A4G-48 A4G-49 A4G-50 A4G-51 A4G-52 A4G-53 A4G-54 A4G-55 A4G-56
1314
SDTRYELVVDKSRLRGKNPTKGKAEQTQTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDRDVEVEAFQRYSEKVH
1390
A4G-57 A4G-58 A4G-59 A4G-60 A4G-61 A4G-62 A4G-63 A4G-64 A4G-65 A4G-66
1391
TSLYECPIESSPLFLLHKKGKNSSKPKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSHCHLFSSPRAIEHAYQYGGT
1467
A4G-67 A4G-68 A4G-69 A4G-70 A4G-71 A4G-72 A4G-73 A4G-74 A4G-75
1468
ANSRQEFEHEQGDFGEKSQFSIRLKTRSSHGMIFYVSDQEENDFMTLFLAHGRLVFMFNVGHKKLKIRSQEKYNDGL
1544
A4G-76 A4G-77 A4G-78 A4G-79 A4G-80 A4G-81 A4G-82 A4G-83 A4G-84 A4G-85
1545
WHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGGVAPGRAVKNVQITSVYSFSGCLGNLQLNGASIT
1621
A4G-86 A4G-87 A4G-88 A4G-89 A4G-90 A4G-91 A4G-92 A4G-93 A4G-94
1622
SASQTFSVTPCFEGPMETGTYFSTEGGYVVLDESFNIGLKFEIAPEVRPRSSSGTLVHGHSVNGEYLNVHMRNGQVI
1698
A4G-95 A4G-96 A4G-97 A4G-98 A4G-99 A4G-100 A4G-101 A4G-102 A4G-103
1699
VKVNNGVRDFSTSVTPKQNLCDGRWHRITVIRDSNVVQLDVDSEVNHVVGPLNPKPVDHREPVFVGGVPESLLTPRL
1775
A4G-104 A4G-105 A4G-106 A4G-107 A4G-108 A4G-109 A4G-110 A4G-111 A4G-112
1776
APSKPFTGCIRHFVIDSRPVSFSKAALVSGAVSINSCPTA
1815
A4G-113 A4G-114 A4G-115 A4G-116

Figure 6

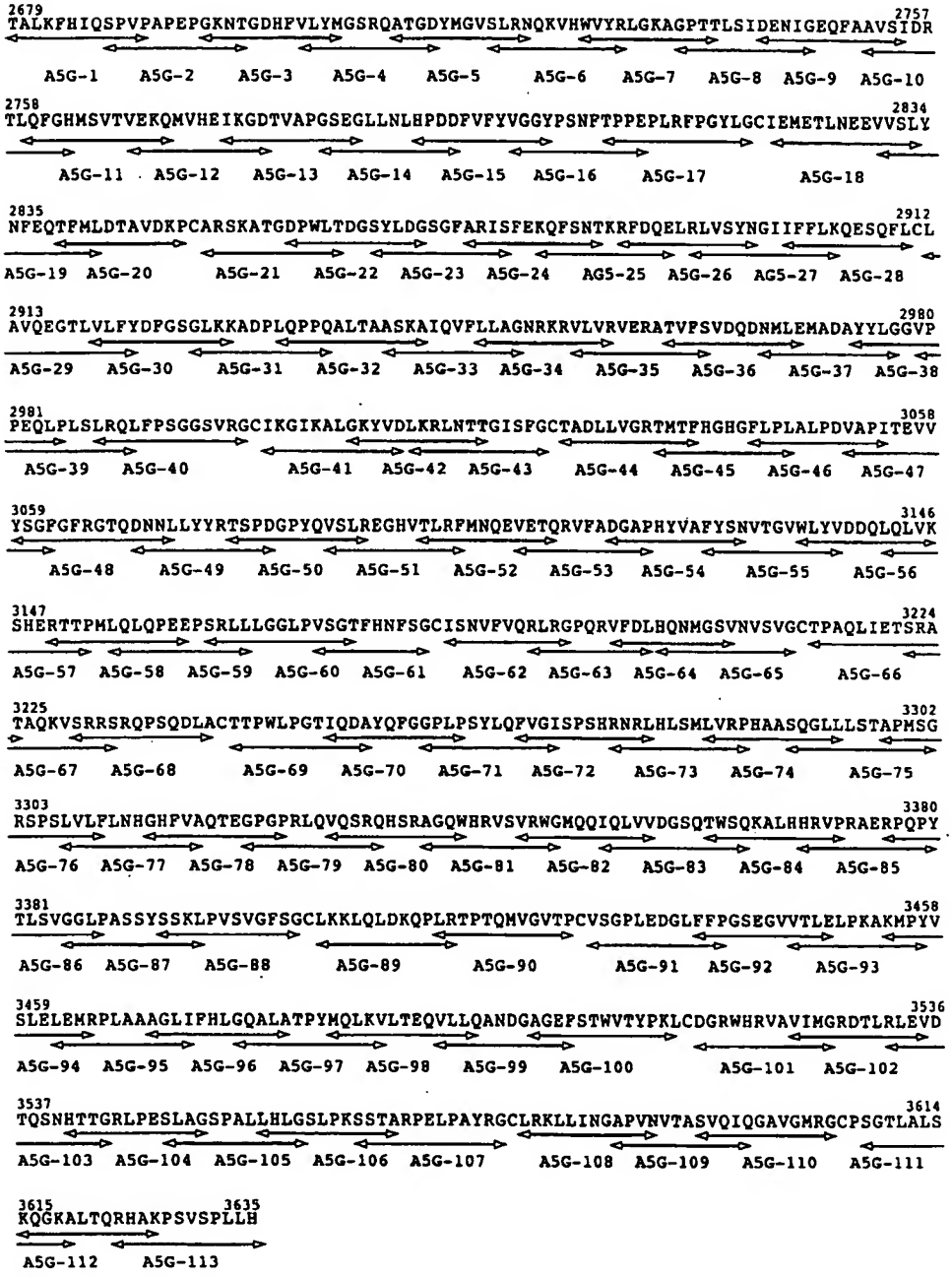

2679
TALKFHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDYMGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQFAAVSIDR
2757
A5G-1 A5G-2 A5G-3 A5G-4 A5G-5 A5G-6 A5G-7 A5G-8 A5G-9 A5G-10
2758
TLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPGYLGCIEMETLNEEVVSLY
2834
A5G-11 A5G-12 A5G-13 A5G-14 A5G-15 A5G-16 A5G-17 A5G-18
2835
NFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQFSNTKRFDQELRLVSYNGIIFFLKQESQFLCL
2912
A5G-19 A5G-20 A5G-21 A5G-22 A5G-23 A5G-24 AG5-25 A5G-26 AG5-27 A5G-28
2913
AVQEGTLVLFYDPGSGLKKADPLQPPQALTAASKAIQVFLLAGNRKRVLVRVERATVFSVDQDNMLEMADAYYLGGVP
2980
A5G-29 A5G-30 A5G-31 A5G-32 A5G-33 A5G-34 A5G-35 A5G-36 A5G-37 A5G-38
2981
PEQLPLSLRQLFPSGGSVRGCIKGIKALGKYVDLKRLNTTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVV
3058
A5G-39 A5G-40 A5G-41 A5G-42 A5G-43 A5G-44 A5G-45 A5G-46 A5G-47
3059
YSGFGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVK
3146
A5G-48 A5G-49 A5G-50 A5G-51 A5G-52 A5G-53 A5G-54 A5G-55 A5G-56
3147
SHERTTPMLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNMGSVNVSVGCTPAQLIETSRA
3224
A5G-57 A5G-58 A5G-59 A5G-60 A5G-61 A5G-62 A5G-63 A5G-64 A5G-65 A5G-66
3225
TAQKVSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPMSG
3302
A5G-67 A5G-68 A5G-69 A5G-70 A5G-71 A5G-72 A5G-73 A5G-74 A5G-75
3303
RSPSLVLFLNHGHFVAQTEGPGPRLQVQSRQHSRAGQWHRVSVRWGMQQIQLVVDGSQTWSQKALHHRVPRAERPQPY
3380
A5G-76 A5G-77 A5G-78 A5G-79 A5G-80 A5G-81 A5G-82 A5G-83 A5G-84 A5G-85
3381
TLSVGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLELPKAKMPYV
3458
A5G-86 A5G-87 A5G-88 A5G-89 A5G-90 A5G-91 A5G-92 A5G-93
3459
SLELEMRPLAAAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEPSTWVTYPKLCDGRWHRVAVIMGRDTLRLEVD
3536
A5G-94 A5G-95 A5G-96 A5G-97 A5G-98 A5G-99 A5G-100 A5G-101 A5G-102
3537
TQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVTASVQIQGAVGMRGCPSGTLALS
3614
A5G-103 A5G-104 A5G-105 A5G-106 A5G-107 A5G-108 A5G-109 A5G-110 A5G-111
3615
KQGKALTQRHAKPSVSPLLH
3635
A5G-112 A5G-113

Figure 7

PEPTIDES	Laminin Chain and Amino Acid Sequence Number	Amino Acid Sequence	% Disruption/ Disassembly of Fibrillar Aß (Aß:Peptide Molar Ratio of 1:6)
AG73	Alpha-1 chain; residues 2719-2730	RKRLQVQLSIRT	46 % (S; $p < 0.01$)***
A3	Alpha-3 chain; residues 2243-2254	KPRLQFSLDIQT	23 % (S; $p < 0.01$)
A5	Alpha-5 chain; residues 3275-3286	RNRLHLSMLVRP	22 % (S; $p<0.01$)
C-16	Gamma-1 chain; residues 139-150	KAFDITYVRLKF	28 % (S; $p<0.01$)***
LAM-L	Alpha-1 chain; residues 2097-2108	AASIKVAVSADR	24 % (S; $p<0.01$)
A-13	Alpha-1 chain; residues 97-109	RQVFQVAYIIIKA	30 % (S; $p<0.01$)***
HA3G45	Alpha-3 chain; residues 1173-1184	ASFGFQTFQPSG	21 % (S; $p<0.05$)
HA3G47	Alpha-3 chain; residues 1189-2000	HQTWTRNLQVTL	28 % (S; $p<0.01$)***
HA3G58	Alpha-3 chain; residues 1276-1287	ISNVFVQRLSLS	32 % (S; $p<0.01$)***
HA3G67	Alpha-3 chain; residues 1342-1353	ASPPSVKVWQDA	25 % (S; $p<0.01$)***
HA3G71	Alpha-3 chain; residues 1379-1390	FKLPQELLKPRS	23 % (S; $p<0.05$)
HA3G74	Alpha-3 chain; residues 1402-1414	RGLVFHTGTKNSF	32 % (S; $p<0.01$)***
HA3G75	Alpha-3 chain; residues 1411-1422	KNSFMALYLSKG	24 % (S; $p<0.01$)
HA3G76	Alpha-3 chain; residues 1418-1429	YLSKGRLVFALG	26 % (S; $p<0.01$)***
HA3G79	Alpha-3 chain; residues 1444-1455	NDGKWHTVVFGH	27 % (S; $p<0.01$)***
HA3G83	Alpha-3 chain; residues 1477-1487	GNSTISIRAPVY	33 % (S; $p<0.01$)***
A4G31	Alpha-4 chain; residues 1101-1112	LHVFYDFGFSNG	23 % (S; $p<0.01$)
A4G82	Alpha-4 chain; residues 1513-1524	TLFLAHGRLVFM	30 % (S; $p<0.01$)***
A5G15	Alpha-5 chain; residues 2792-2803	HPDDFVFYVGGY	30 % (S; $p<0.01$)***
A5G35	Alpha-5 chain; residues 2950-2961	VLVRVERATVFS	20 % (S; $p<0.05$)
A5G46	Alpha-5 chain; residues 3043-3054	FLPLALPDVAPI	21 % (S; $p<0.05$)
A5G56	Alpha-5 chain; residues 3135-3146	WLYVDDQLQLVK	27 % (S; $p<0.01$)***
A5G71	Alpha-5 chain; residues 3259-3270	GPLPSYLQFVGI	22 % (S; $p<0.05$)
A5G80	Alpha-5 chain; residues 3329-3340	VQSRQHSRAGQW	25 % (S; $p<0.01$)***
A5G81	Alpha-5 chain; residues 3337-3348	AGQWHRVSVRWG	41 % (S; $p<0.01$)***
A5G82	Alpha-5 chain; residues 3345-3356	VRWGMQQIQLVV	29 % (S; $p<0.01$)***
A5G84	Alpha-5 chain; residues 3361-3372	TWSQKALHHRVP	27 % (S; $p<0.01$)***
A5G101	Alpha-5 chain; residues 3516-3527	DGRWHRVAVIMG	39 % (S; $p<0.01$)***
A5G109	Alpha-5 chain; residues 3587-3598	APVNVTASVQIQ	32 % (S; $p<0.01$)***
A5G110	Alpha-5 chain; residues 3594-3605	SVQIQGAVGMRG	23 % (S; $p<0.05$)

*** Selected for Further Testing

Figure 8

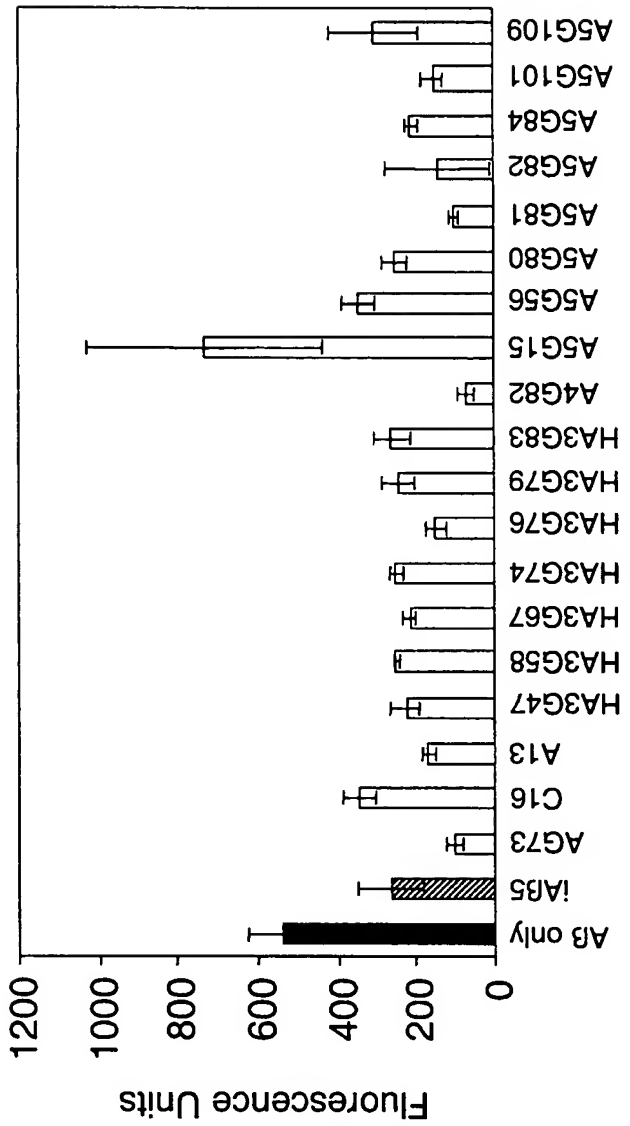

Fluorescence Units
0
200
400
600
800
1000
1200
Aβ only
iAβ5
AG73
C16
A13
HA3G47
HA3G58
HA3G67
HA3G74
HA3G76
HA3G79
HA3G83
A4G82
A5G15
A5G56
A5G80
A5G81
A5G82
A5G84
A5G101
A5G109

Figure 9

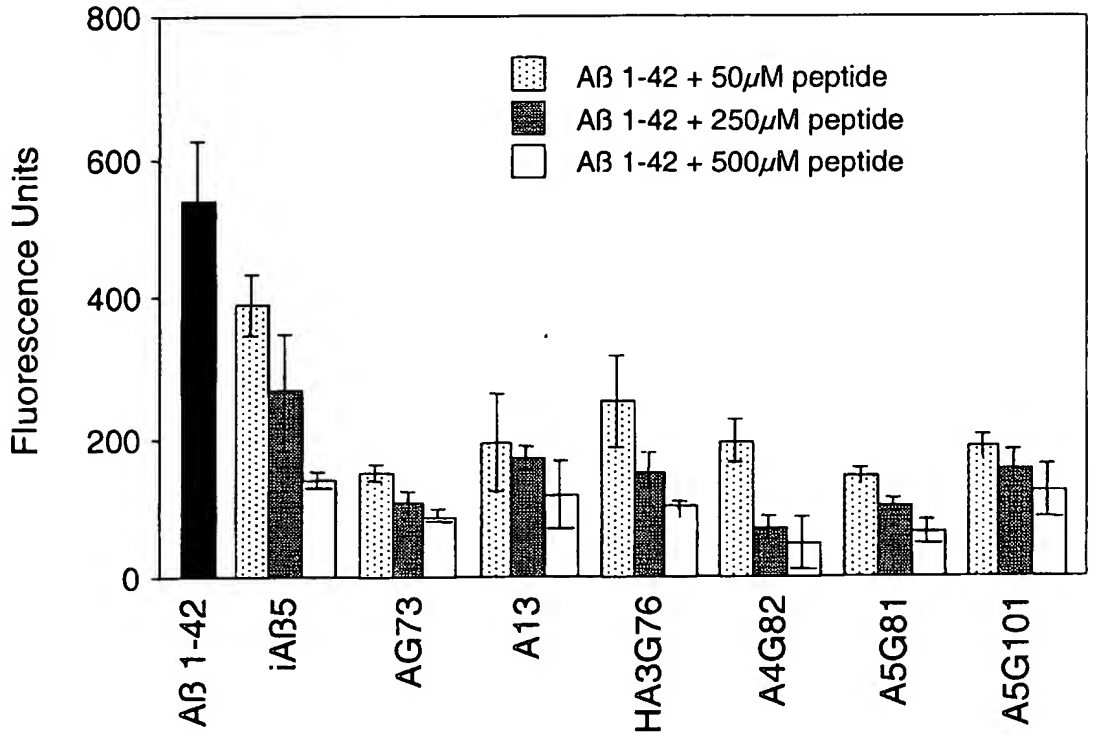

800
600
400
200
0
Fluorescence Units
Aß 1-42 + 50μM peptide
Aß 1-42 + 250μM peptide
Aß 1-42 + 500μM peptide
Aß 1-42
iAß5
AG73
A13
HA3G76
A4G82
A5G81
A5G101

Figure 10

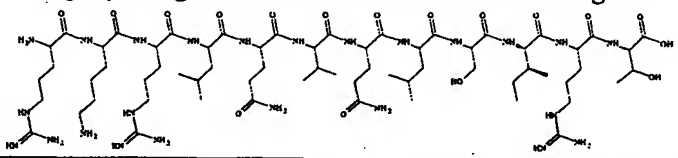
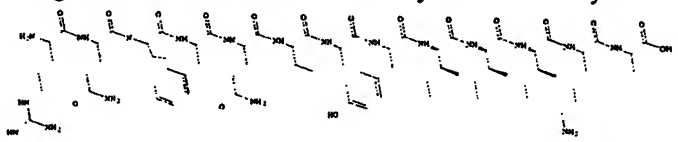
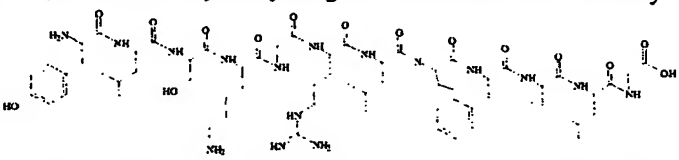
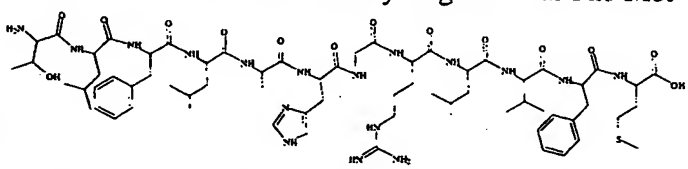
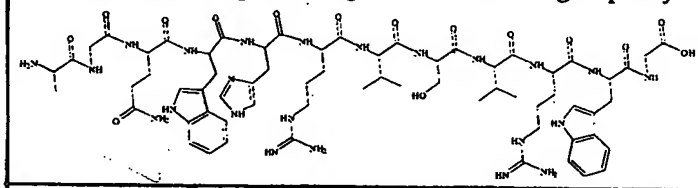
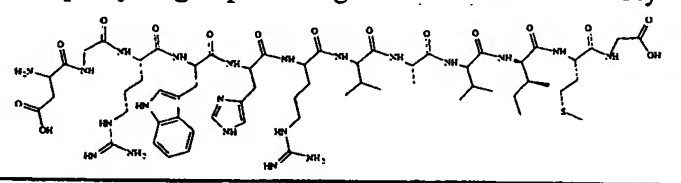
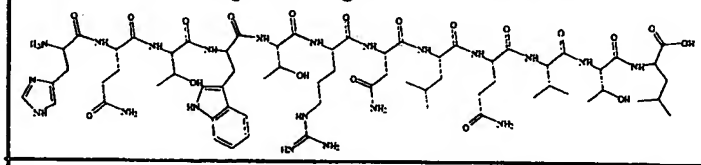
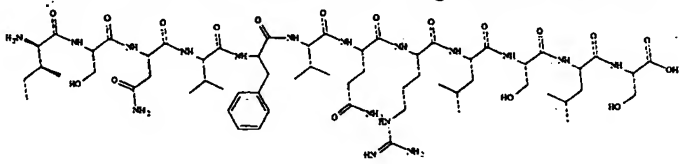
PTI-	Structure	Formula	MW
DP-001 D-AG73 or D-A1 A1-chain 2719-2730	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-002 D-A13 A1-chain 97-109	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-004 D-A4G82 A4-chain 1513-1524	Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
DP-005 D-A5G81 A5-chain 3337-3348	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-006 D-A5G101 A5-chain 3516-3527	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000	His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu 	$C_{66}H_{105}N_{21}O_{19}$	1496.70
DP-008 D-HA3G58 A3-chain 1276-1287	Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser 	$C_{61}H_{103}N_{17}O_{18}$	1362.60

Fig. 12a

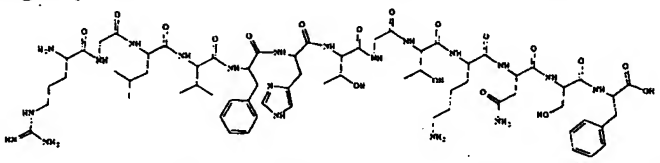
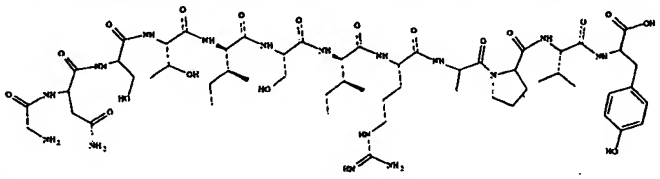
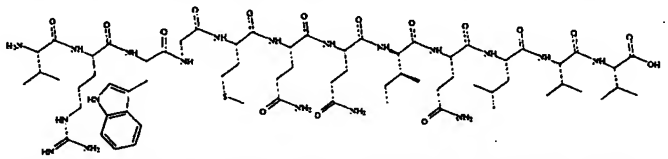
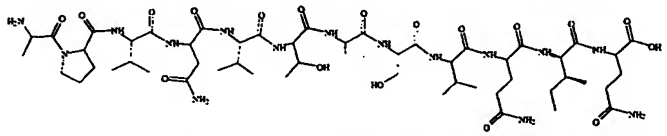
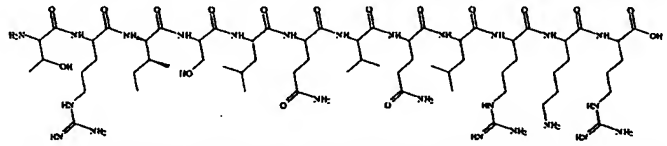
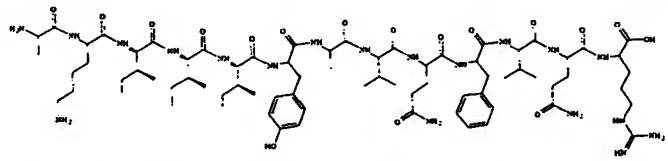
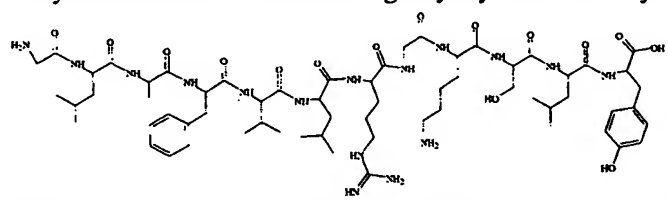
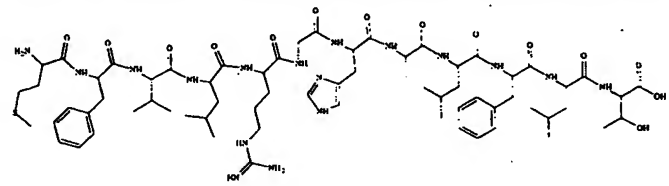
PTI-	Structure	Formula	MW
DP-009 D-HA3G74 A3-chain 1402-1414	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe 	$C_{66}H_{102}N_{20}O_{18}$	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487	Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr 	$C_{56}H_{92}N_{16}O_{18}$	1277.45
DP-011 D-A5G82 A5-chain 3345-3356	Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val 	$C_{66}H_{109}N_{19}O_{16}S$	1456.78
DP-012 D-A5G109 A3-chain 1444-1455	Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln 	$C_{53}H_{91}N_{15}O_{18}$	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719	Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-014 D-rA13 A1-chain r92-109 or 109-92	Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg 	$C_{74}H_{121}N_{19}O_{17}$	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418	Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513	Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75

Fig. 12b

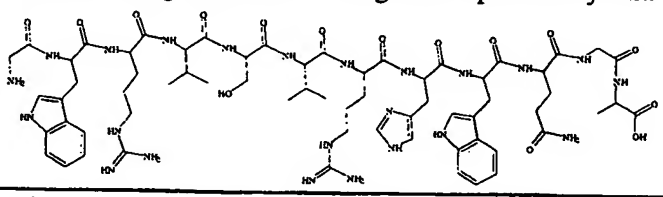
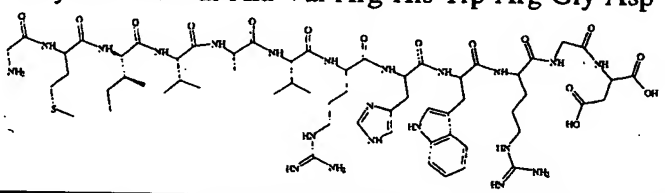
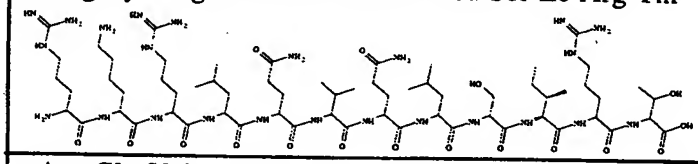
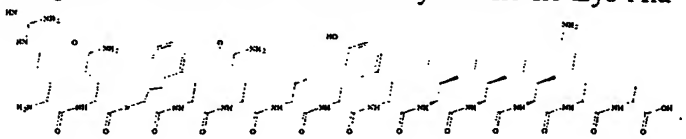
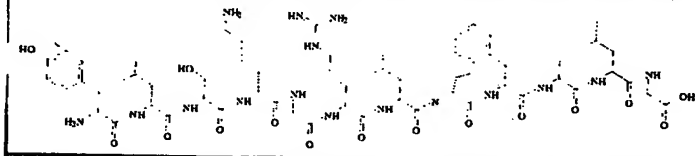
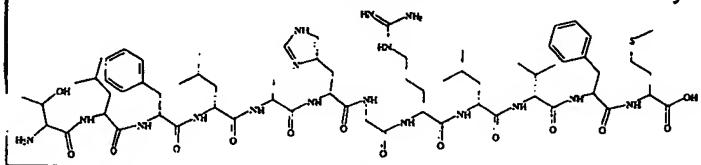
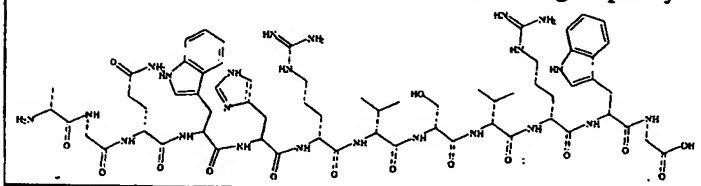
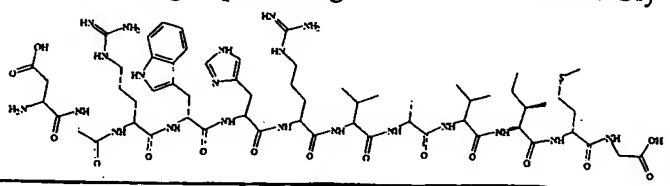
PTI-	Structure	Formula	MW
DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337	Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516	Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
LP-019 AG73 or A1 A1-chain 2719-2730	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
LP-020 A13 A1-chain 92-109	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
LP-021 HA3G76 A3-chain 1418-1429	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
LP-022 A4G82 A4-chain 1513-1524	Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
LP-023 A5G81 A5-chain 3337-3348	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
LP-024 A5G101 A5-chain 3516-3527	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65

Fig. 12c

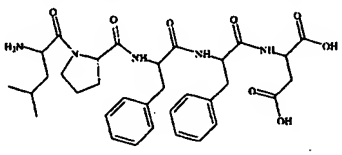
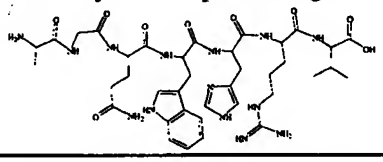
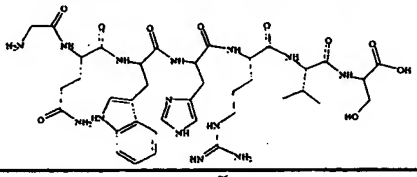
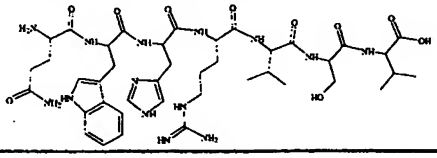
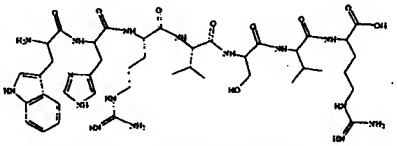
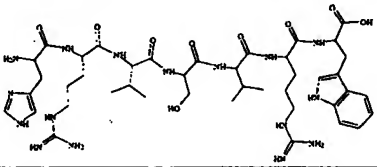
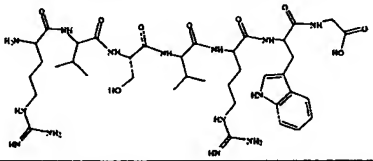
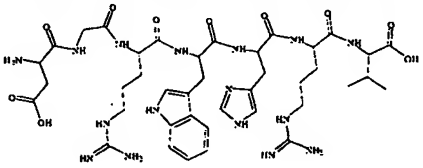
PTI-	Structure	Formula	MW
LP-025 β-sheet breaker or iAβ5	Leu-Pro-Phe-Phe-Asp 	$C_{33}H_{43}N_5O_8$	637.74
DP-026 Trc'n 5;1-7	Ala-Gly-Gln-Trp-His-Arg-Val 	$C_{38}H_{56}N_{14}O_9$	852.95
DP-027 Trc'n 5;2-8	Gly-Gln-Trp-His-Arg-Val-Ser 	$C_{38}H_{56}N_{14}O_{10}$	868.95
DP-028 Trc'n 5;3-9	Gln-Trp-His-Arg-Val-Ser-Val 	$C_{41}H_{62}N_{14}O_{10}$	911.04
DP-029 Trc'n 5;4-10	Trp-His-Arg-Val-Ser-Val-Arg 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-030 Trc'n 5;5-11	His-Arg-Val-Ser-Val-Arg-Trp 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-031 Trc'n 5;6-12	Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{38}H_{62}N_{14}O_9$	859.00
DP-032 Trc'n 6;1-7	Asp-Gly-Arg-Trp-His-Arg-Val 	$C_{40}H_{60}N_{16}O_{10}$	925.02

Fig. 12d

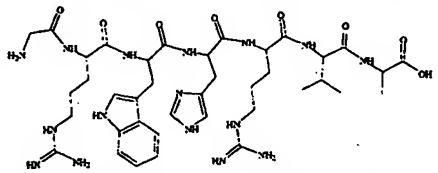
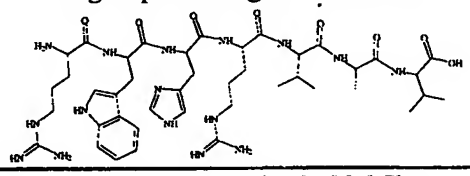
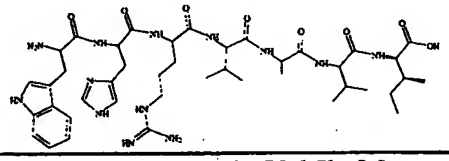
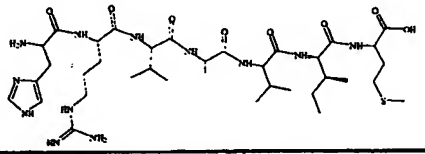
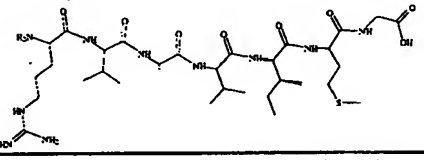
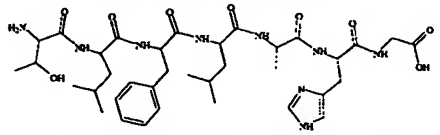
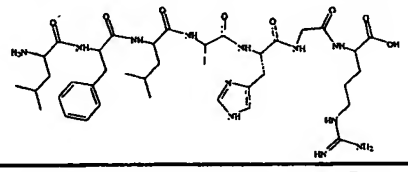
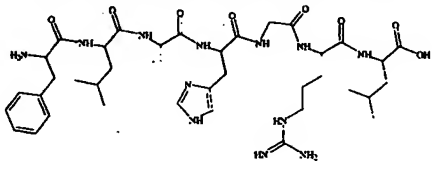
PTI-	Structure	Formula	MW
DP-033 Trc'n 6;2-8	Gly-Arg-Trp-His-Arg-Val-Ala 	$C_{39}H_{60}N_{16}O_8$	881.01
DP-034 Trc'n 6;3-9	Arg-Trp-His-Arg-Val-Ala-Val 	$C_{42}H_{66}N_{16}O_8$	923.09
DP-035 Trc'n 6;4-10	Trp-His-Arg-Val-Ala-Val-Ile 	$C_{42}H_{65}N_{13}O_8$	880.07
DP-036 Trc'n 6;5-11	His-Arg-Val-Ala-Val-Ile-Met 	$C_{36}H_{64}N_{12}O_8S$	825.05
DP-037 Trc'n 6;6-12	Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{32}H_{60}N_{10}O_8S$	744.96
DP-038 Trc'n 4;1-7	Thr-Leu-Phe-Leu-Ala-His-Gly 	$C_{36}H_{55}N_9O_9$	757.89
DP-039 Trc'n 4;2-8	Leu-Phe-Leu-Ala-His-Gly-Arg 	$C_{38}H_{60}N_{12}O_8$	812.97
DP-040 Trc'n 4;3-9	Phe-Leu-Ala-His-Gly-Arg-Leu 	$C_{38}H_{60}N_{12}O_8$	812.98

Fig. 12e

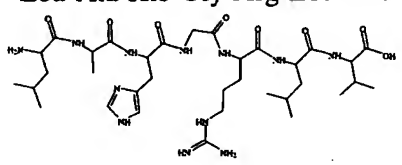
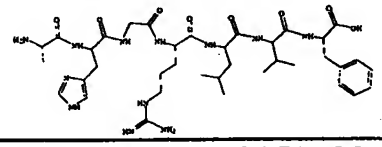
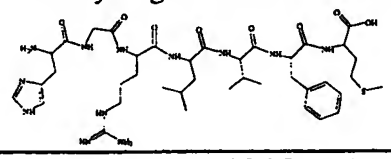
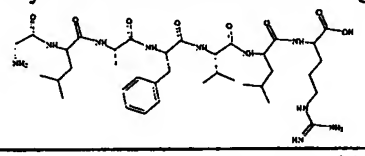
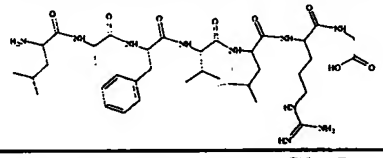
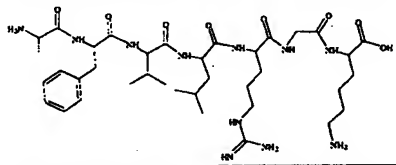
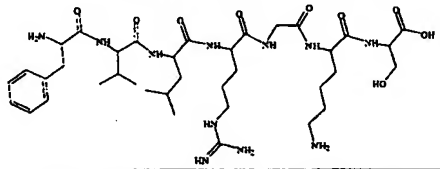
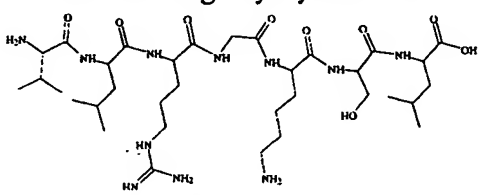
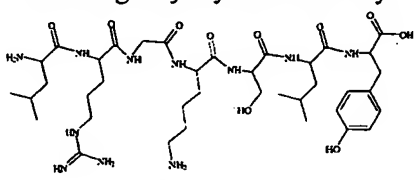
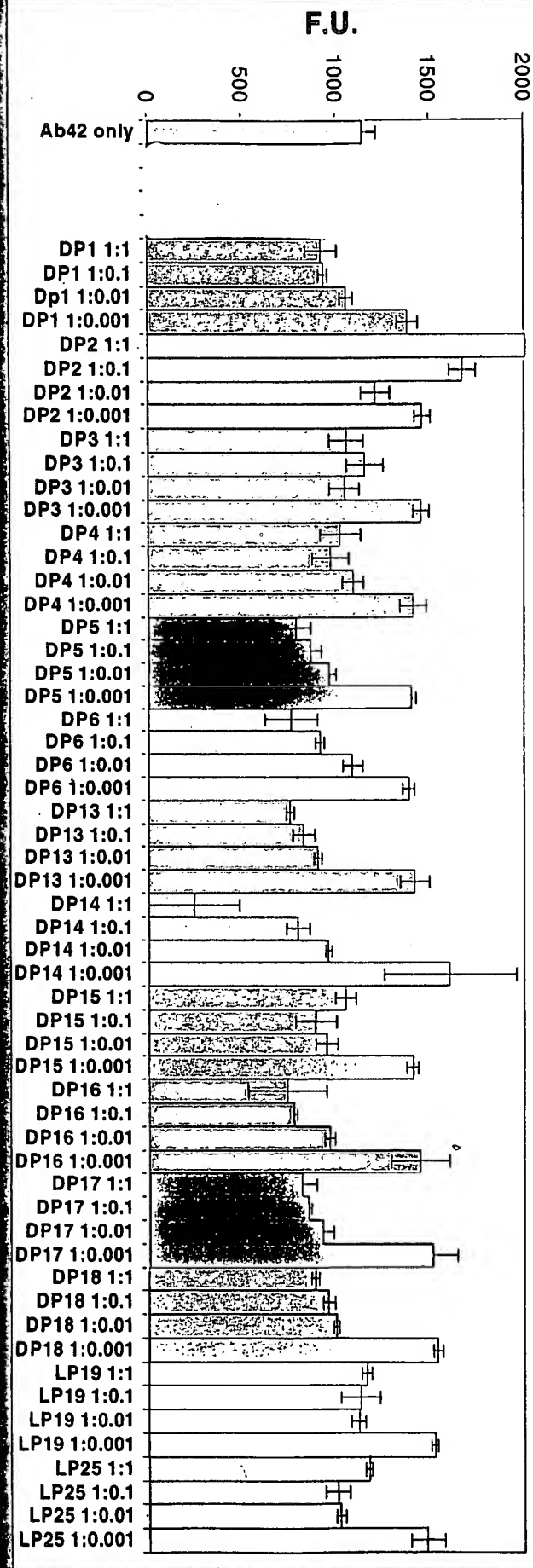
PTI-	Structure	Formula	MW
DP-041 Trc'n 4;4-10	Leu-Ala-His-Gly-Arg-Leu-Val 	$C_{34}H_{60}N_{12}O_8$	764.93
DP-042 Trc'n 4;5-11	Ala-His-Gly-Arg-Leu-Val-Phe 	$C_{37}H_{58}N_{12}O_8$	798.95
DP-043 Trc'n 4;6-12	His-Gly-Arg-Leu-Val-Phe-Met 	$C_{39}H_{62}N_{12}O_8S$	859.07
DP-044 Trc'n 15;1-7	Gly-Leu-Ala-Phe-Val-Leu-Arg 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-045 Trc'n 15;2-8	Leu-Ala-Phe-Val-Leu-Arg-Gly 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-046 Trc'n 15;3-9	Ala-Phe-Val-Leu-Arg-Gly-Lys 	$C_{37}H_{63}N_{11}O_8$	789.98
DP-047 Trc'n 15;4-10	Phe-Val-Leu-Arg-Gly-Lys-Ser 	$C_{37}H_{63}N_{11}O_9$	805.98
DP-048 Trc'n 15;5-11	Val-Leu-Arg-Gly-Lys-Ser-Leu 	$C_{34}H_{65}N_{11}O_9$	771.96
DP-049 Trc'n 15;6-2	Leu-Arg-Gly-Lys-Ser-Leu-Tyr 	$C_{38}H_{65}N_{11}O_{10}$	836.01

Fig. 12f

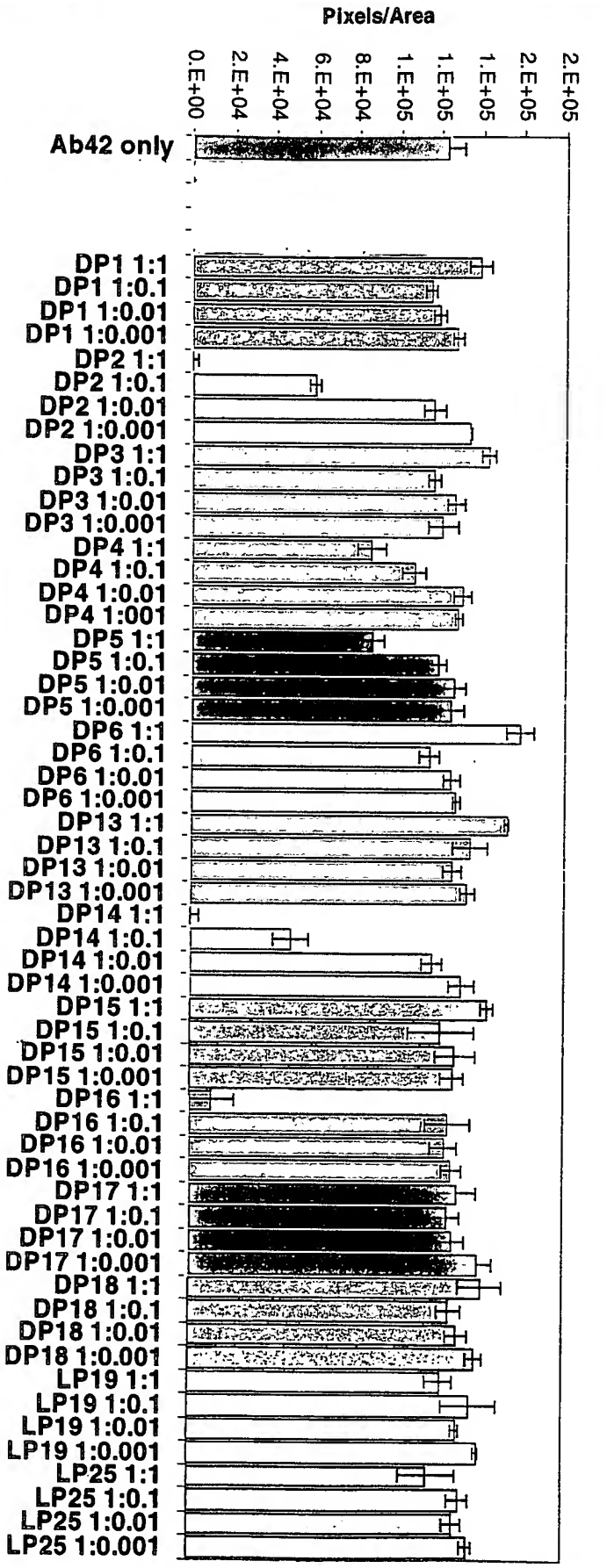
In Vitro Screening of Laminin Peptides



ProteoTech

Fig. 13

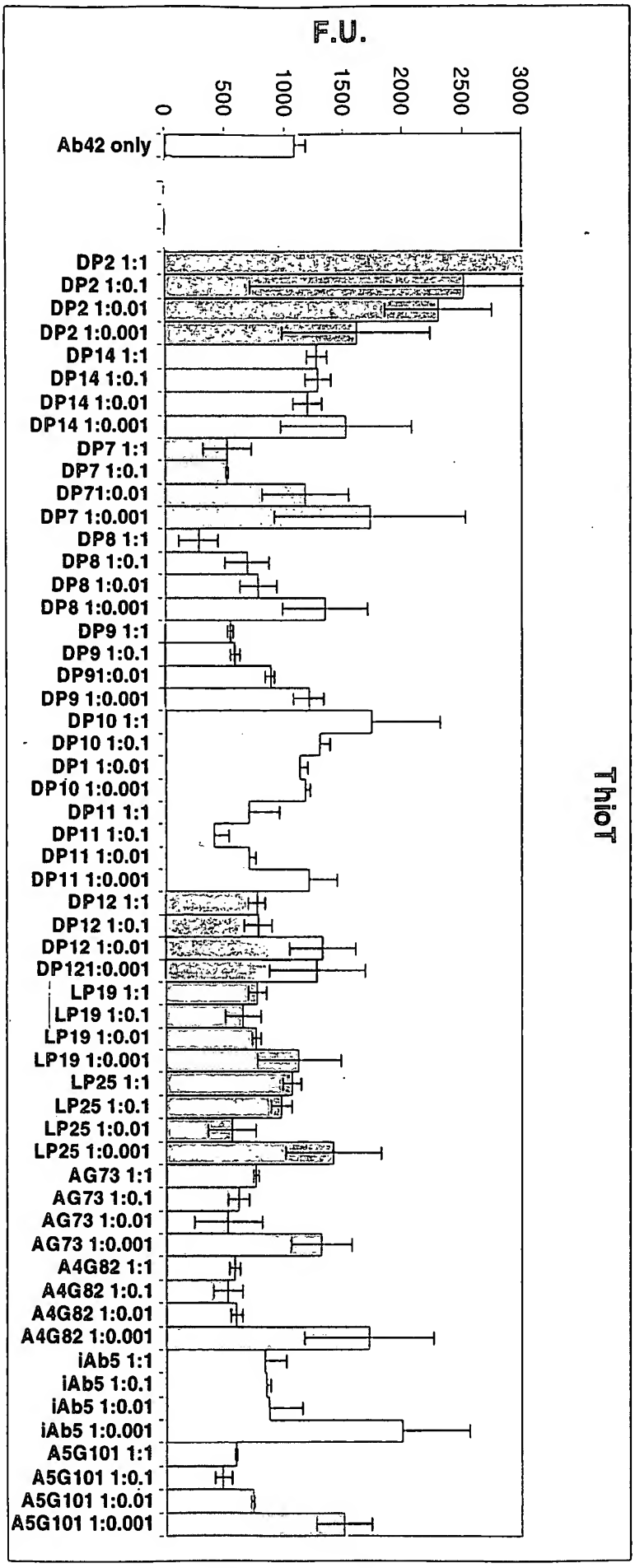
In Vitro Screening of Laminin Peptides



ProteoTech

Fig. 14

In Vitro Screening of Laminin Peptides



ProteoTech

Fig. 15

In Vitro Screening of Laminin Peptides

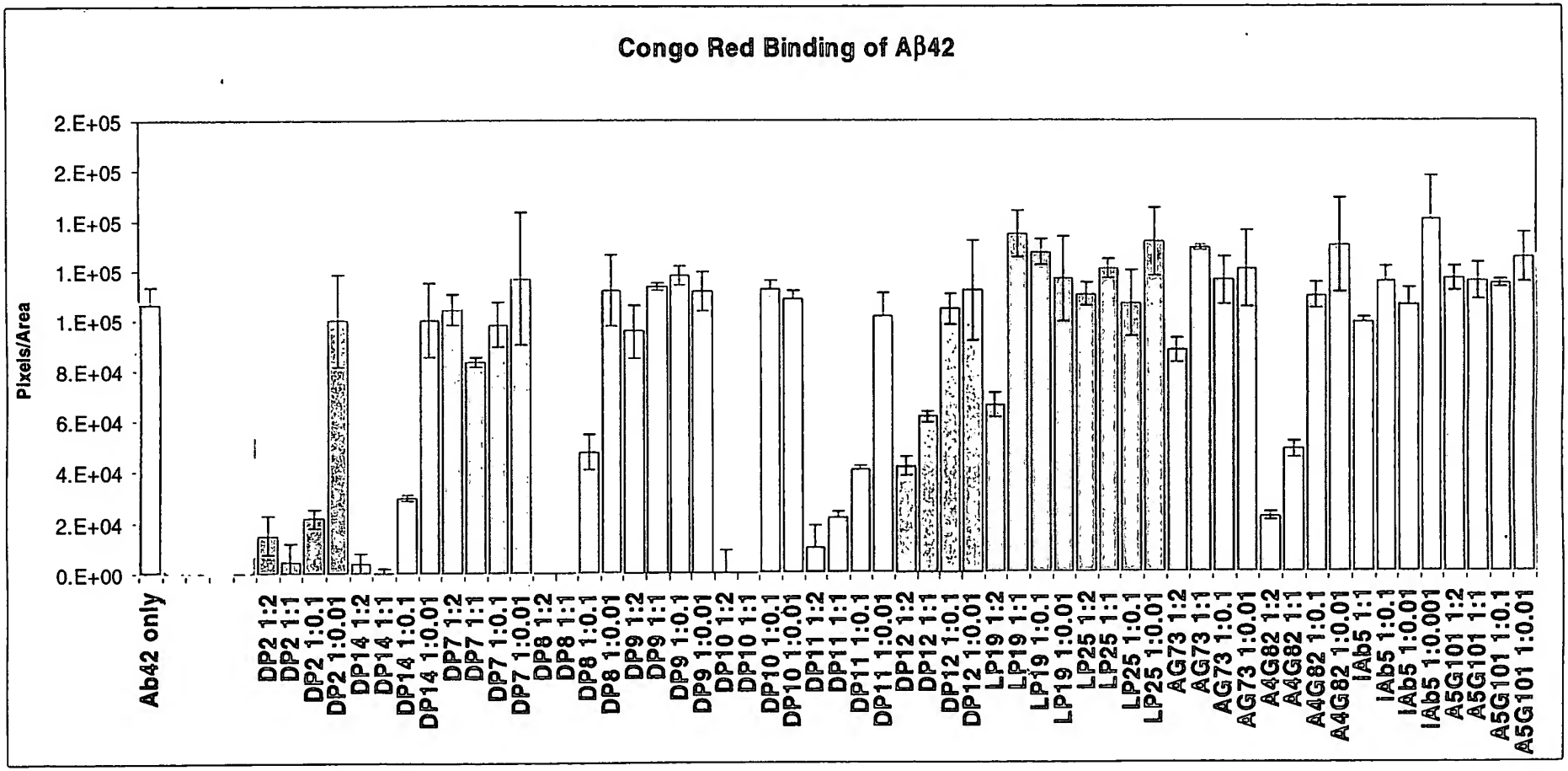
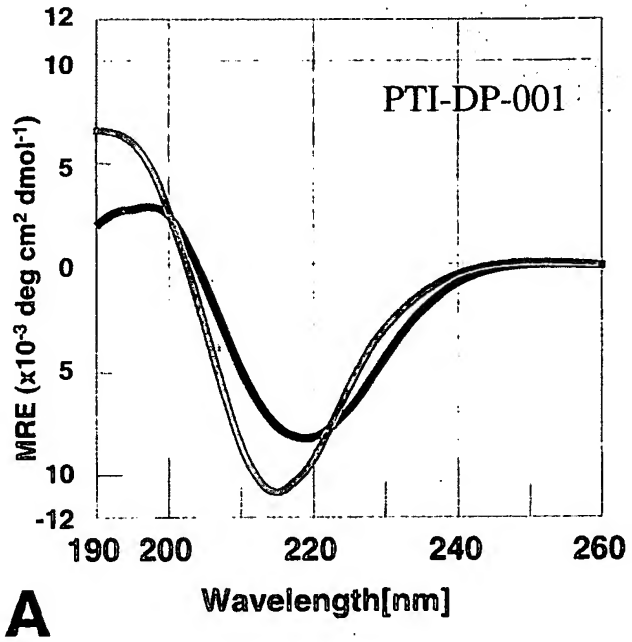
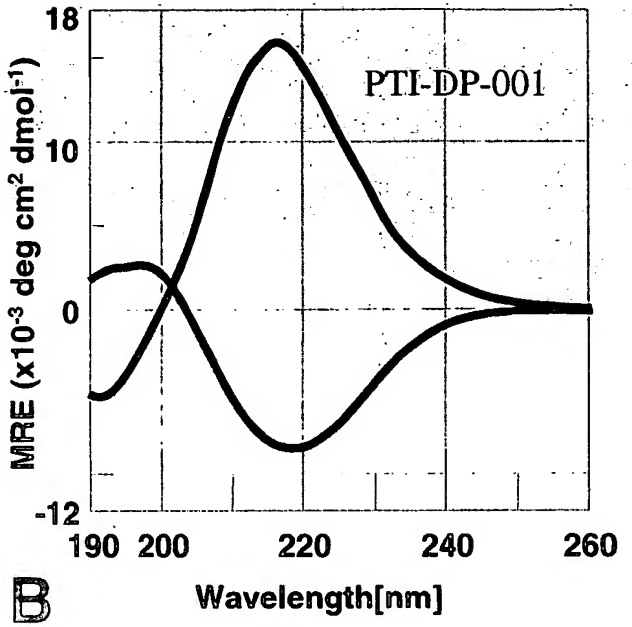


Fig. 14

ProteoTech



A



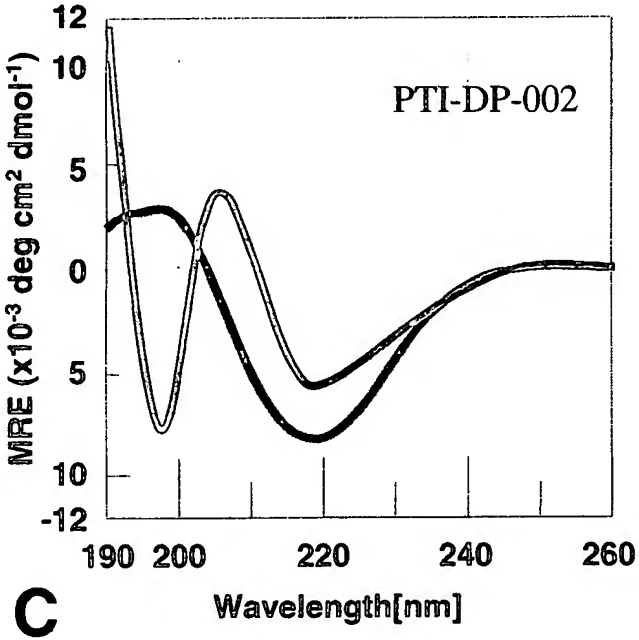
B

Legend:

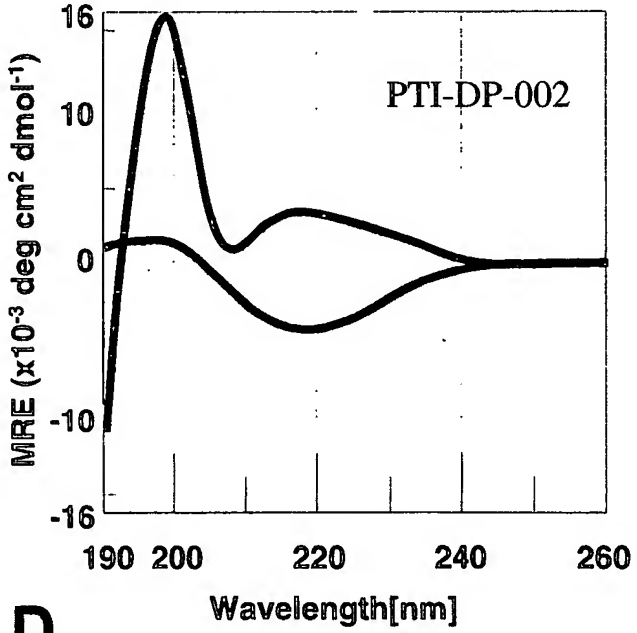
Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



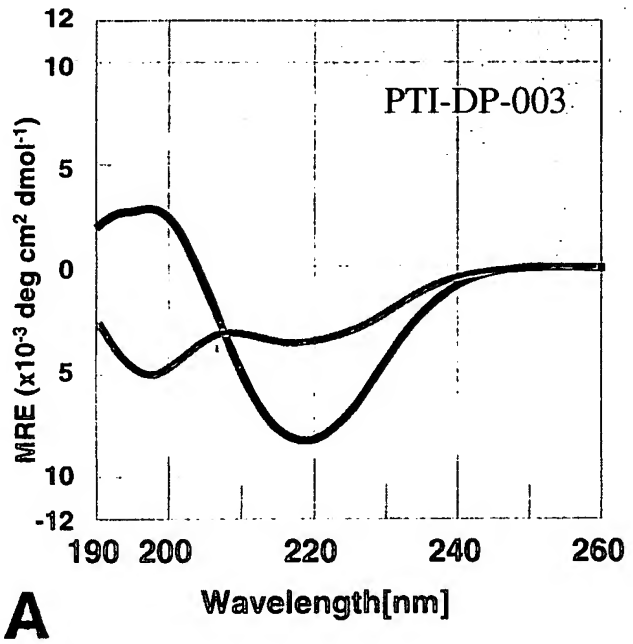
C



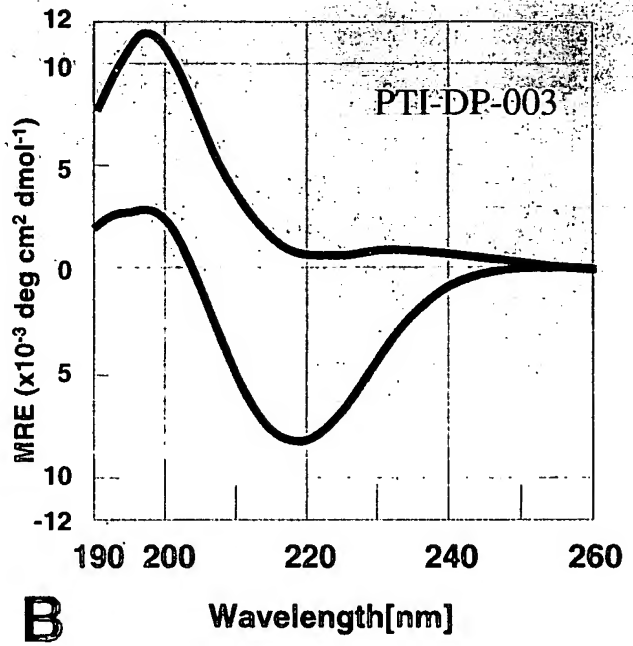
D

CD#34

Fig. 17



A



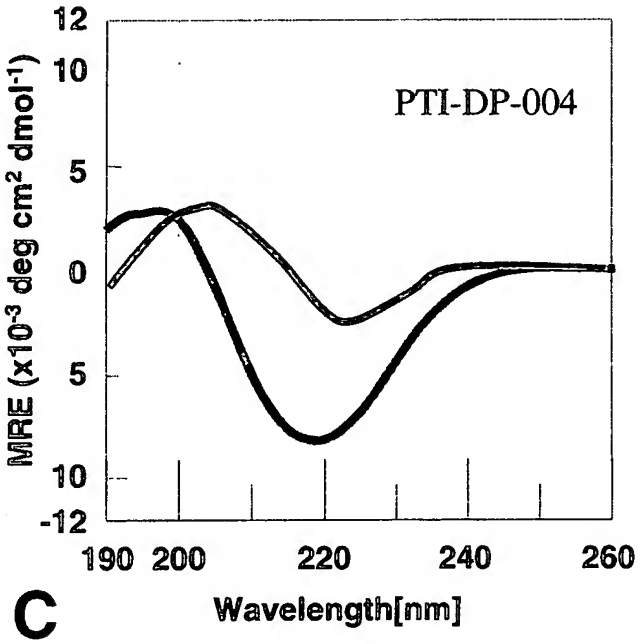
B

Legend:

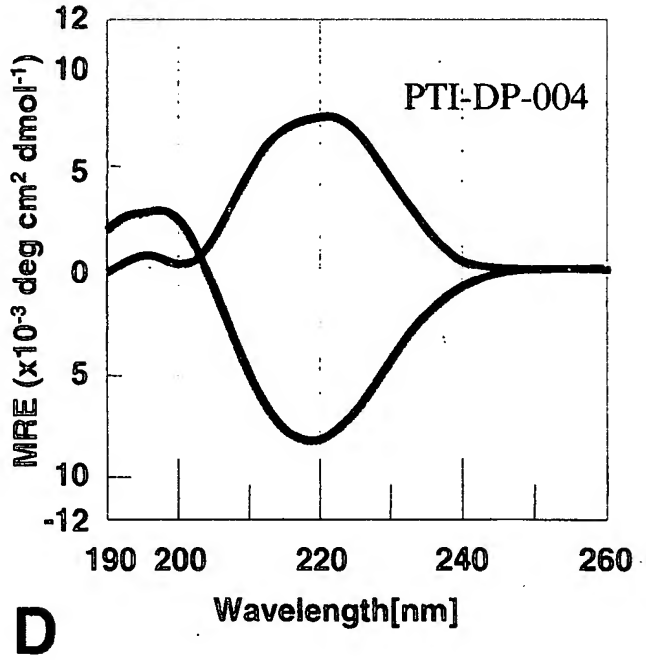
Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



C

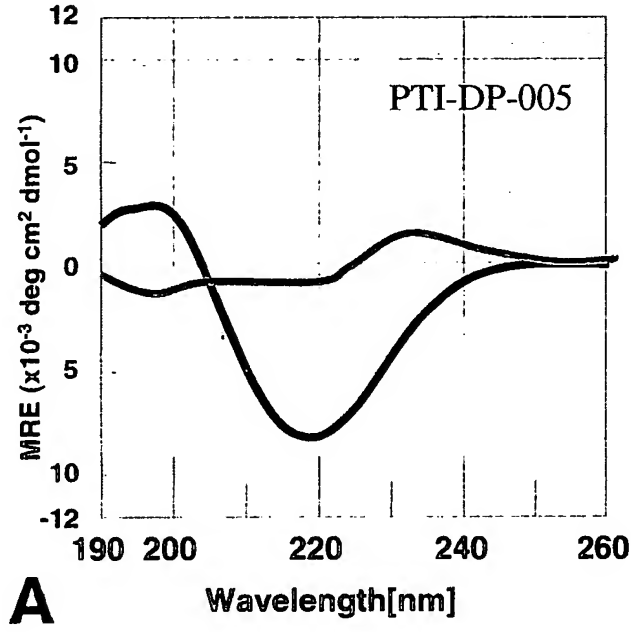


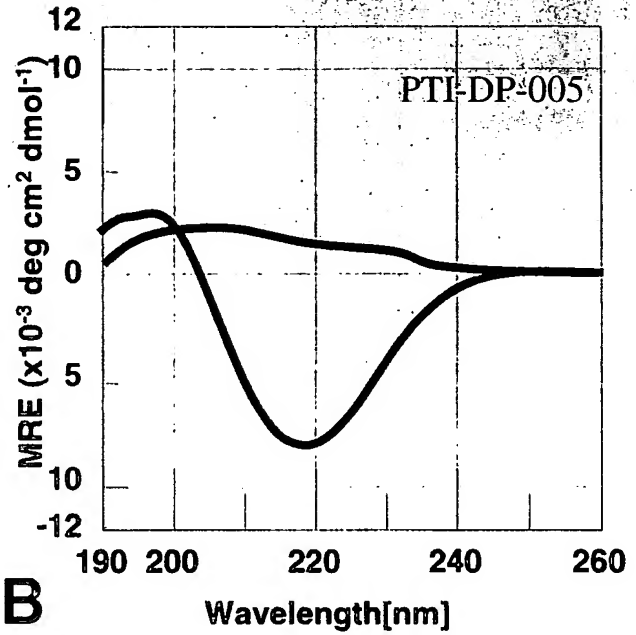
D

CD#34

Fig 18

Fig. 14



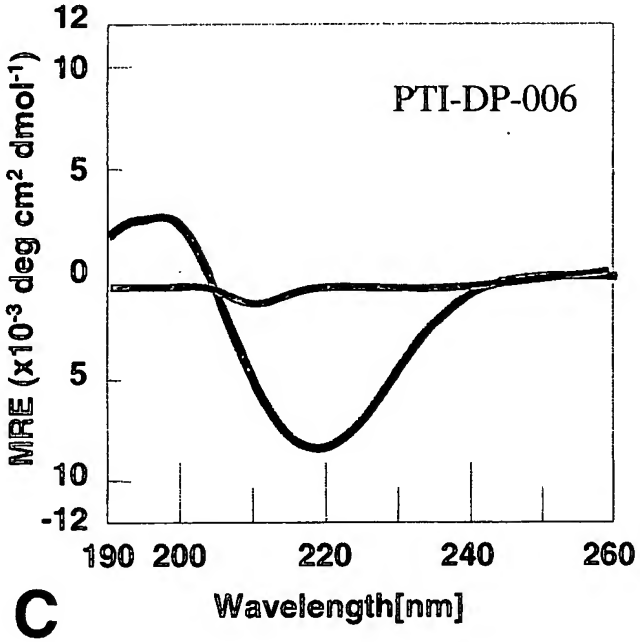


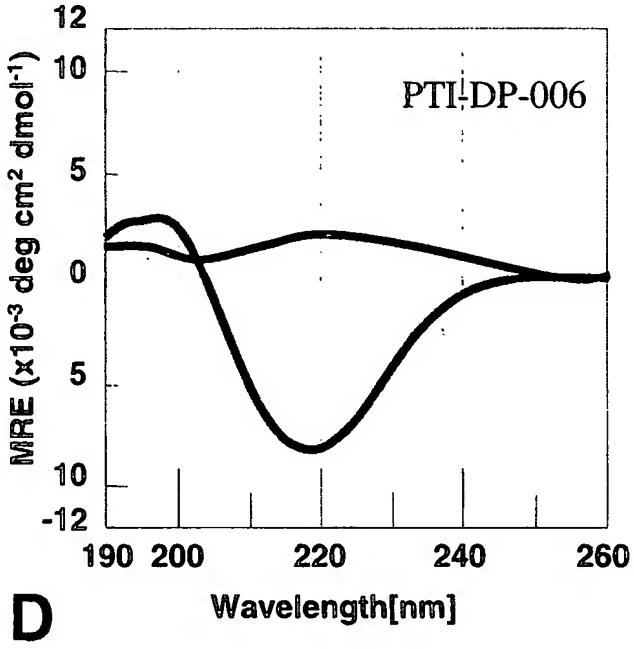
Legend:

Aβ42 Only
0.1 mg/ml

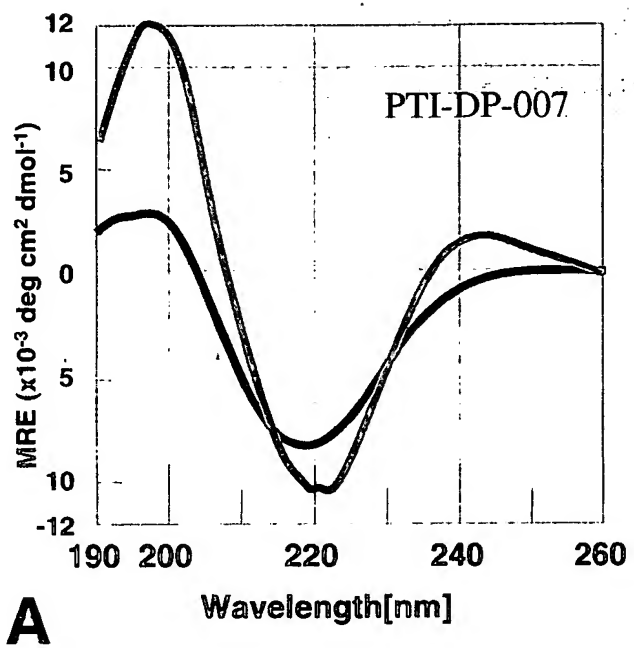
PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt

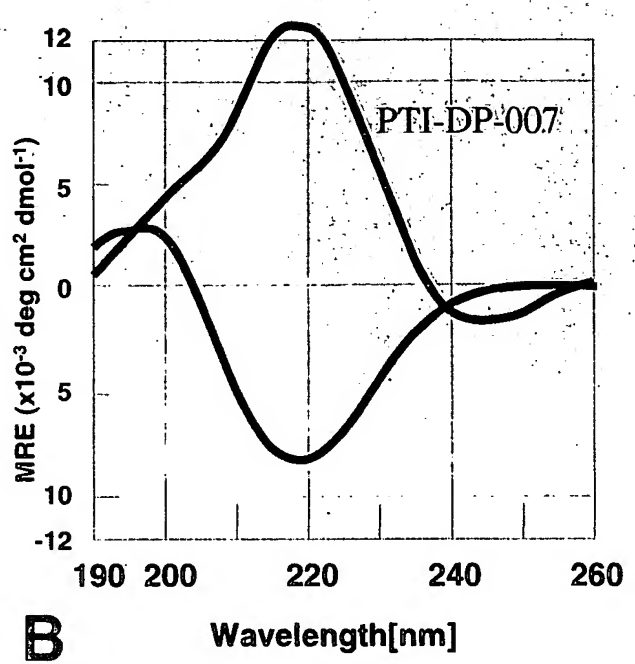




CD#33



A



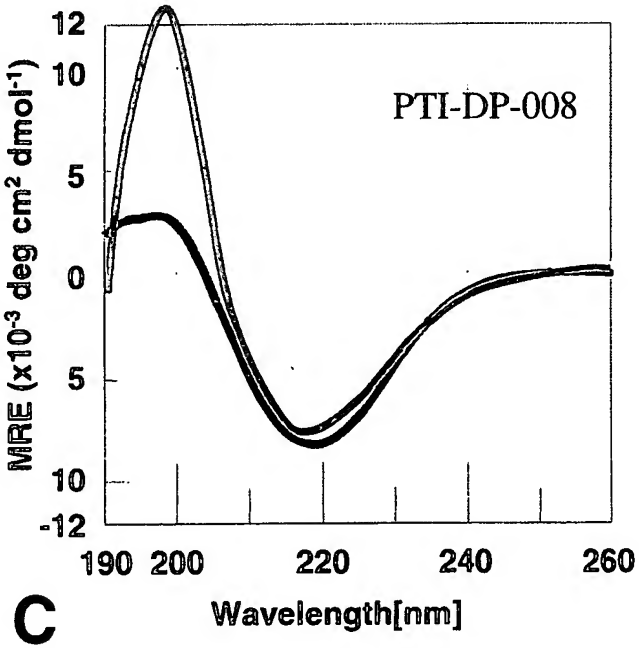
B

Legend:

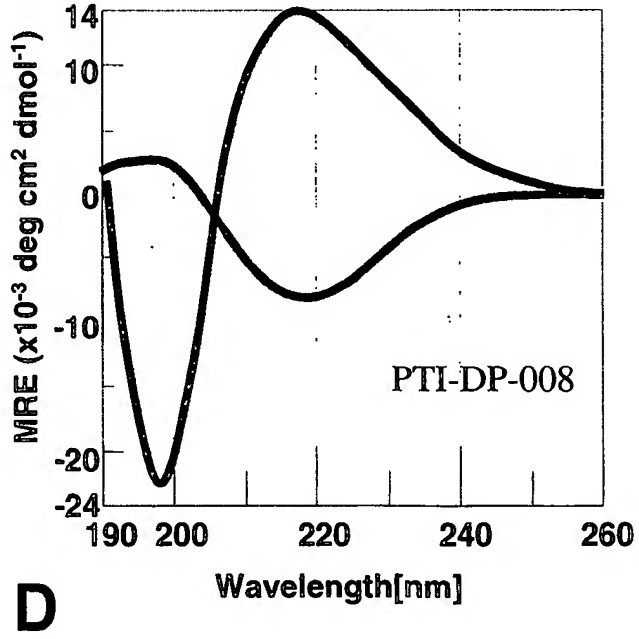
Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



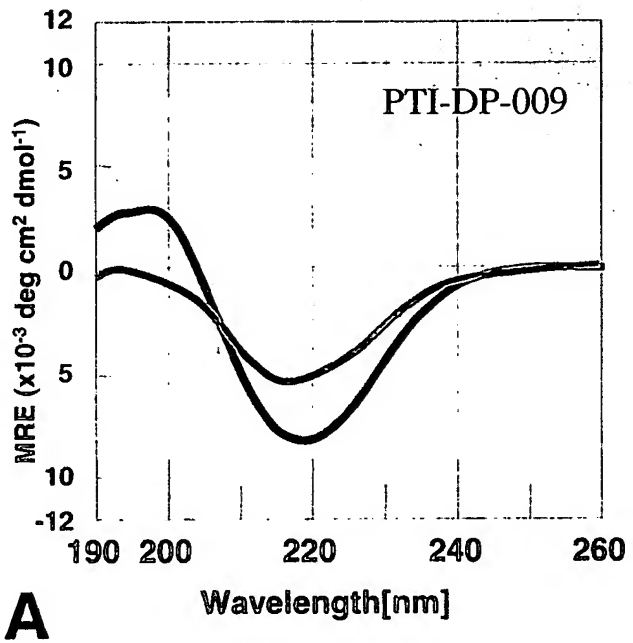
C



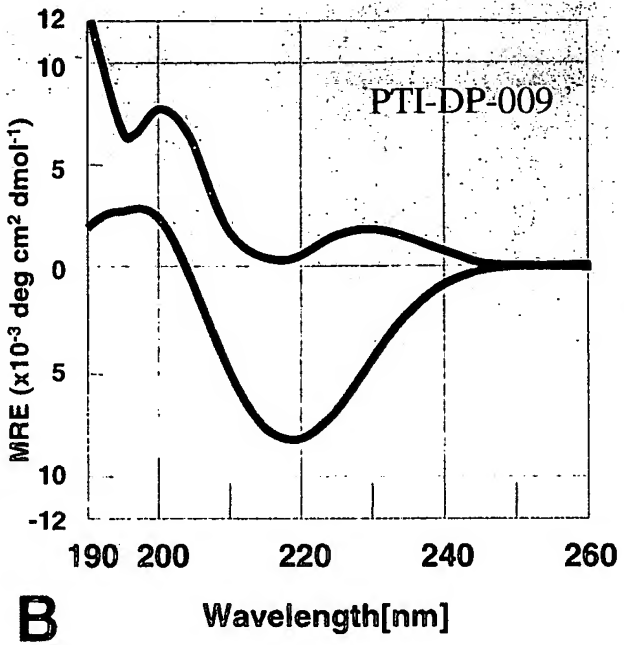
D

CD#34

Fig. 30



A



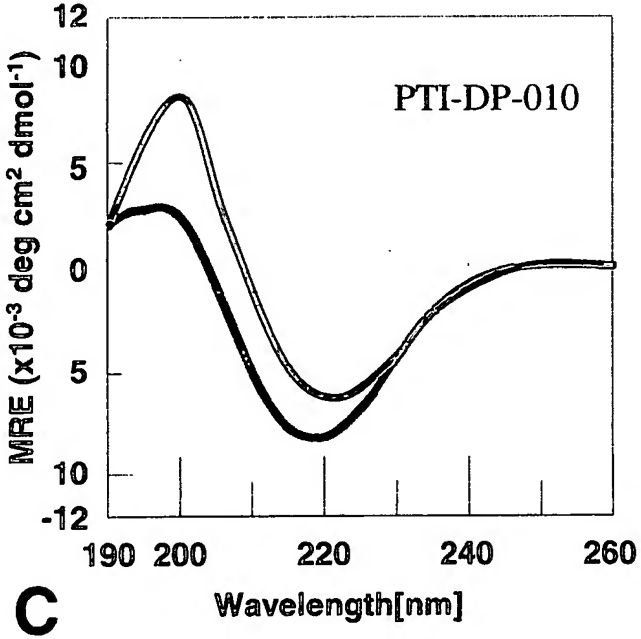
B

Legend:

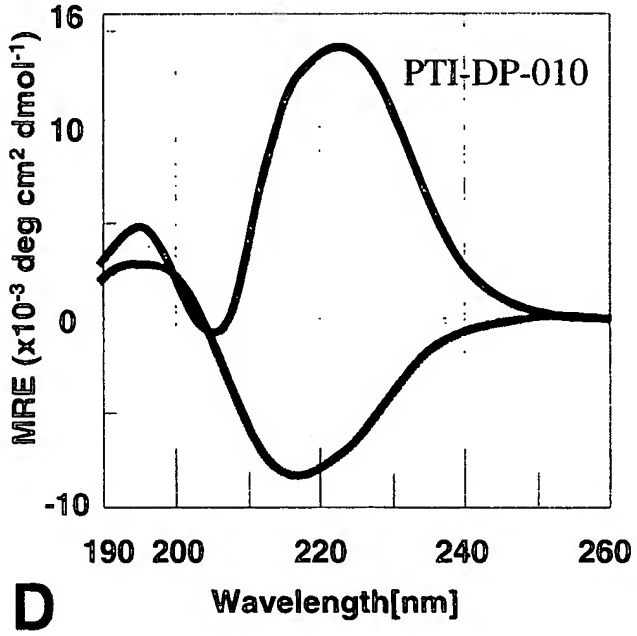
Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



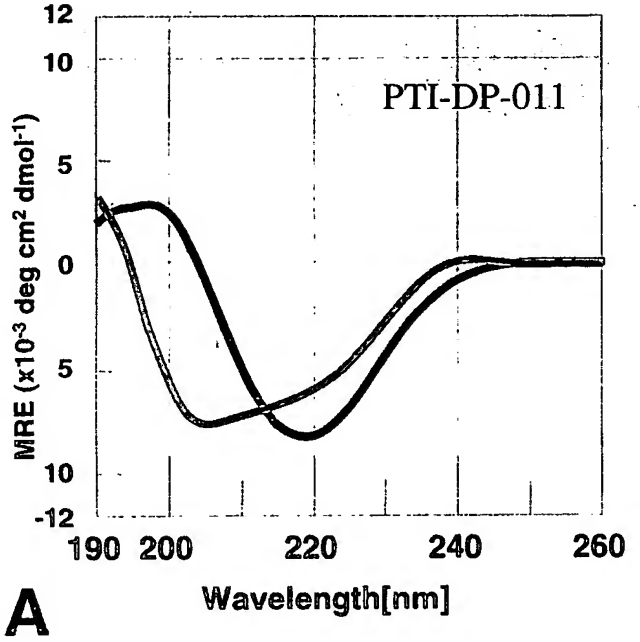
C

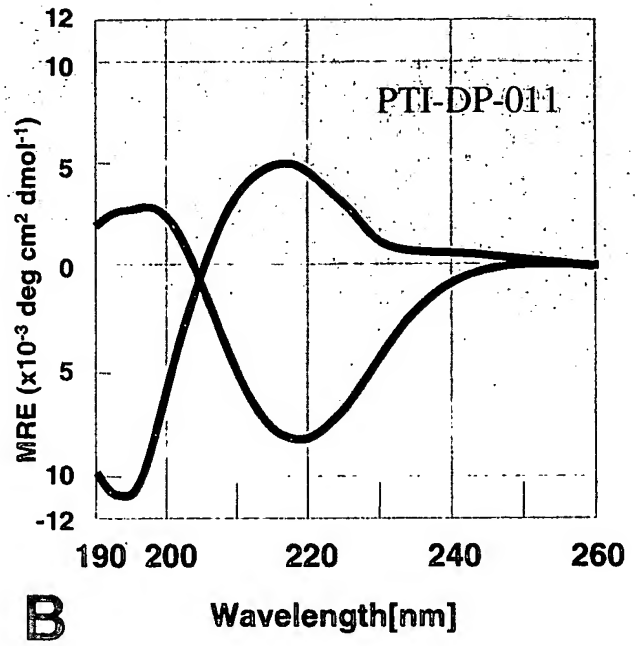


D

Fig. 2a

CD#34



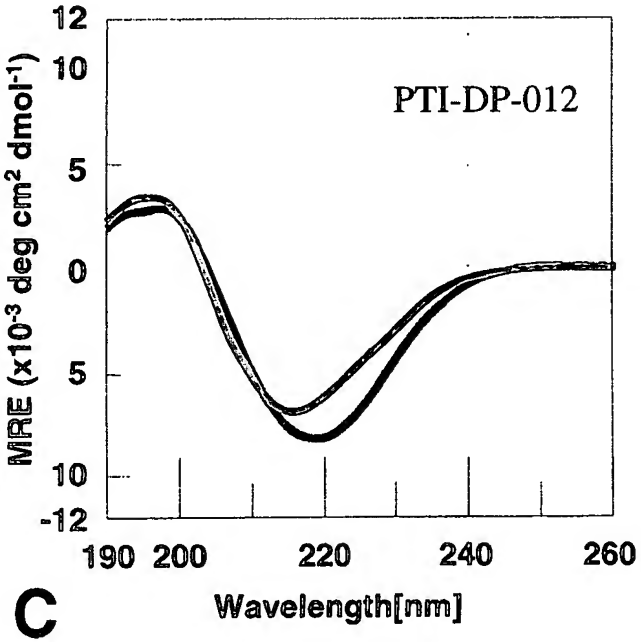


Legend:

Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



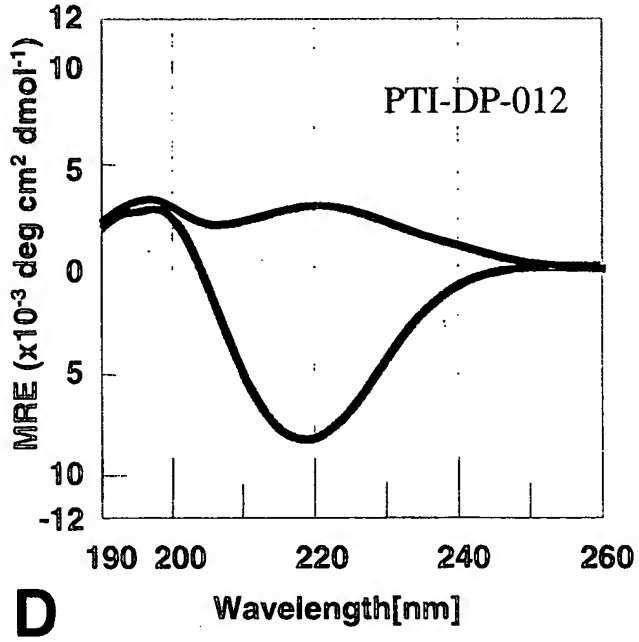
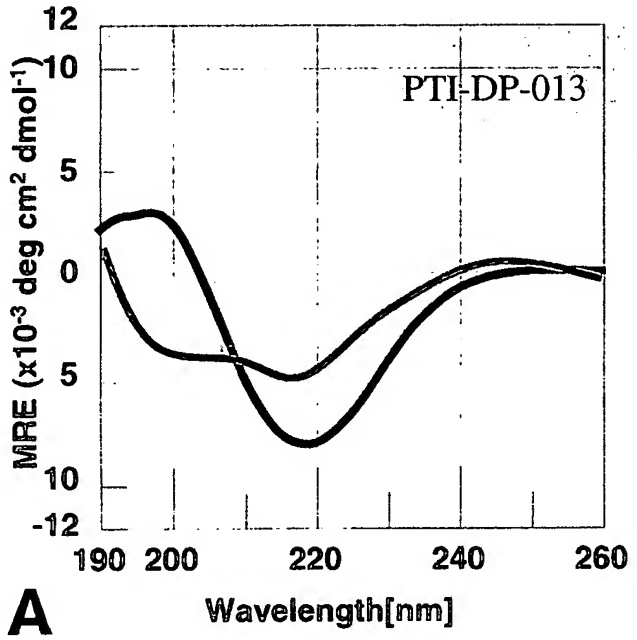
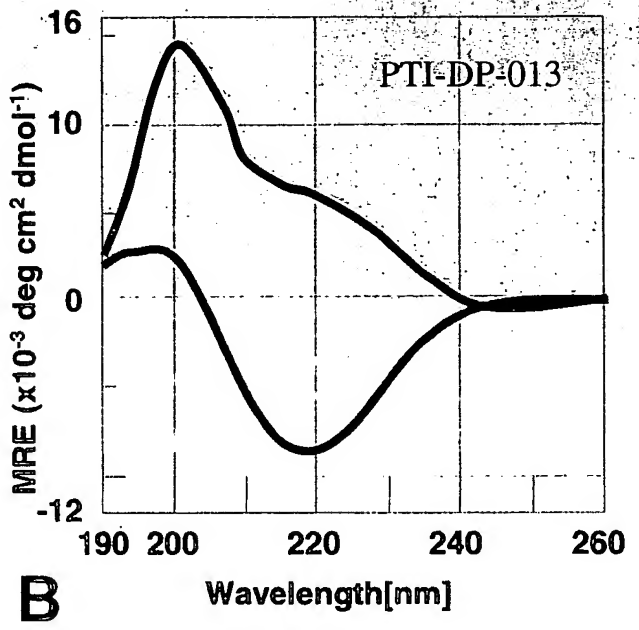


Fig. 22

CD#34



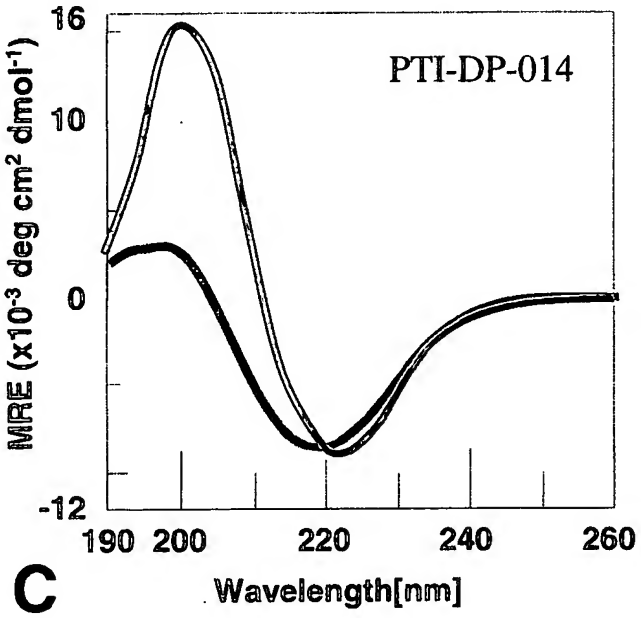


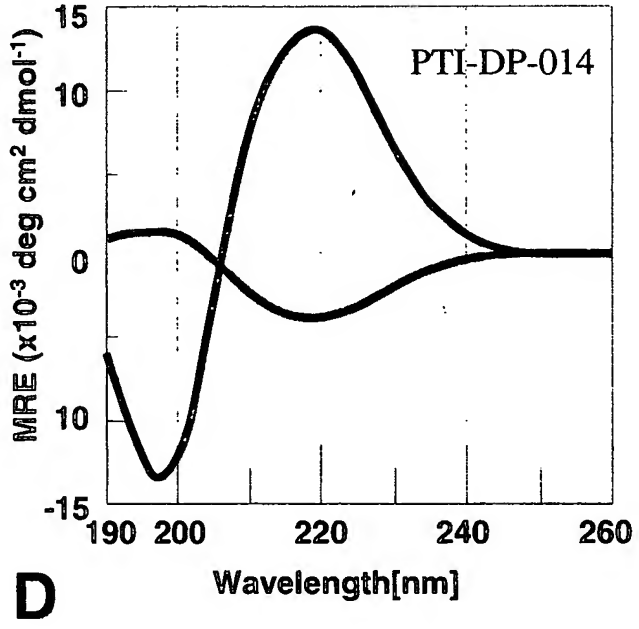
Legend:

Aβ42 Only
0.1 mg/ml

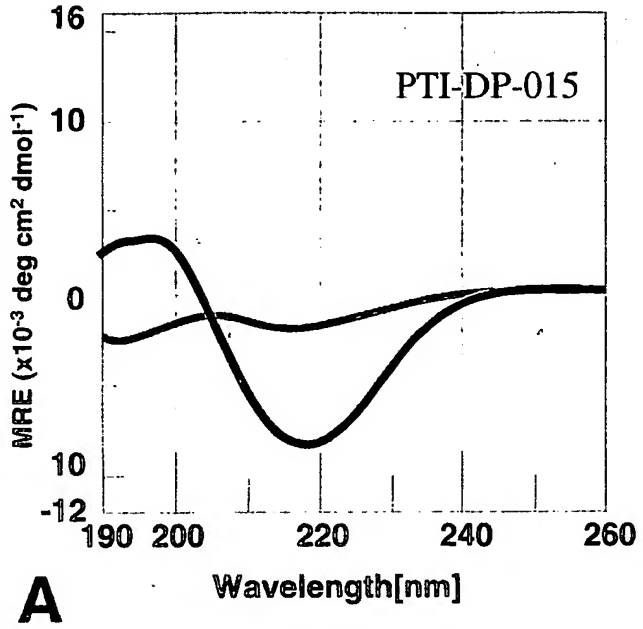
PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt

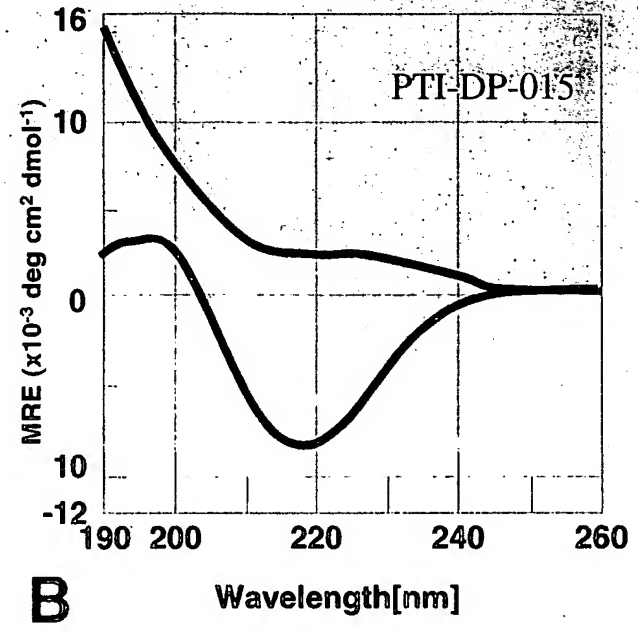




CD#33



A



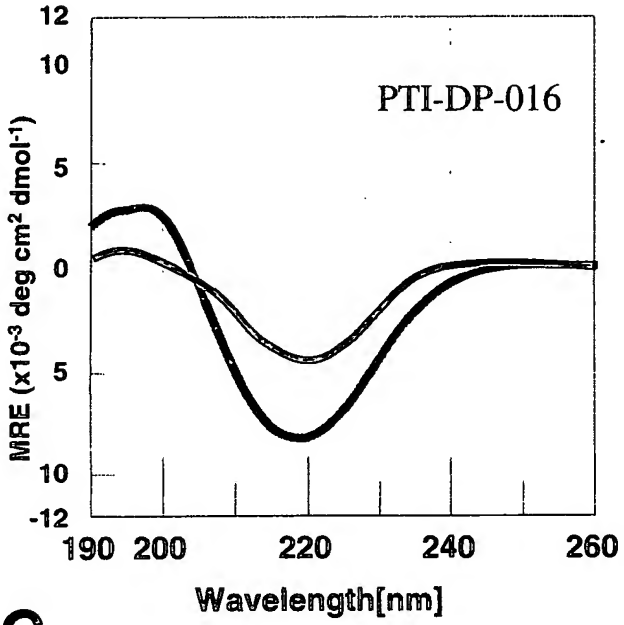
B

Legend:

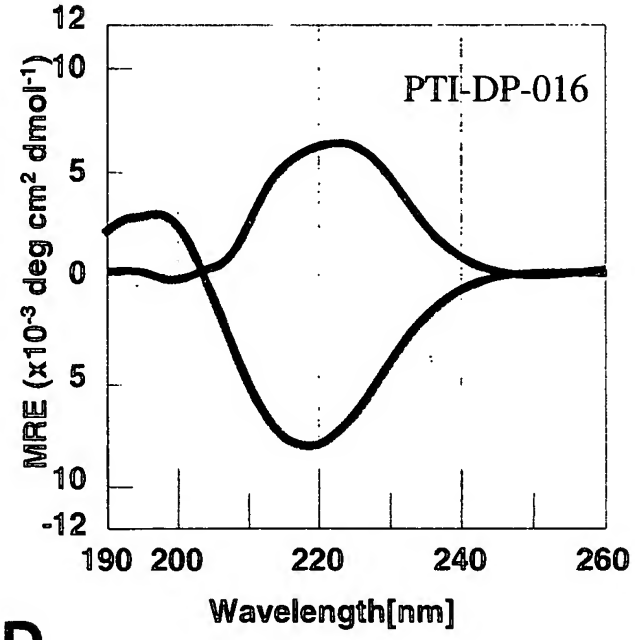
Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



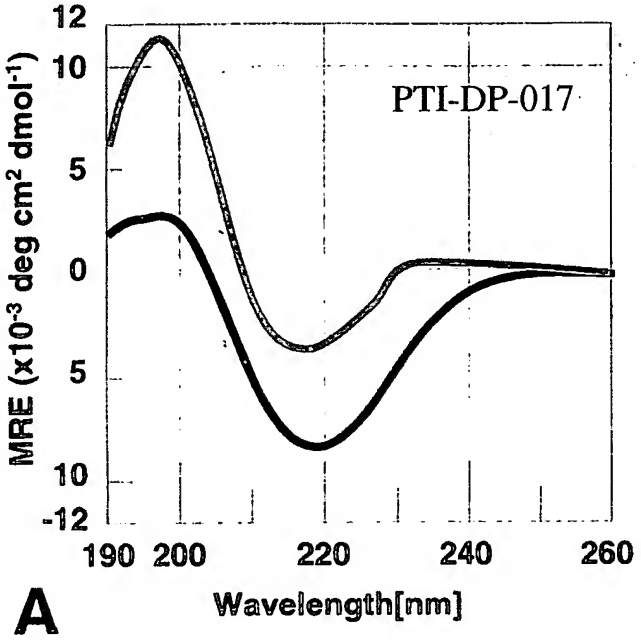
C

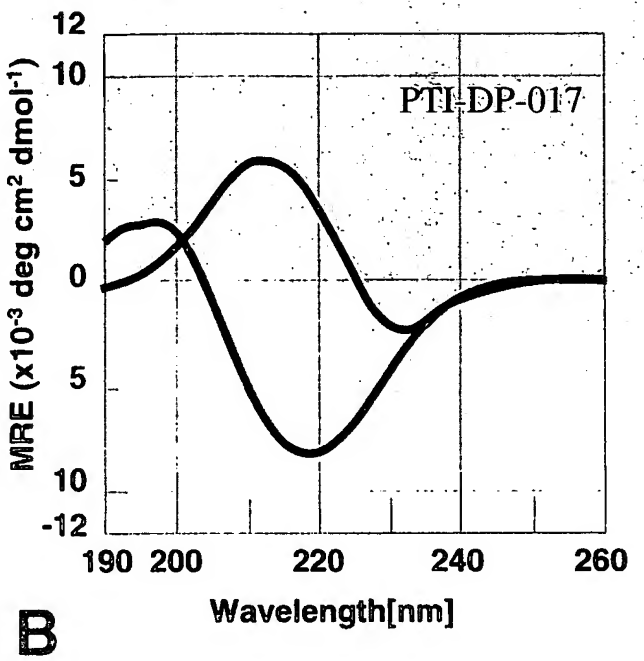


D

Fig. 3H

CD#34



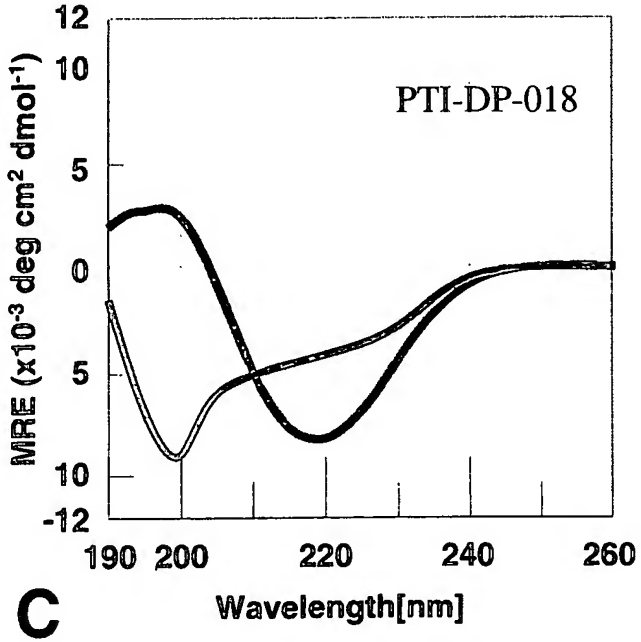


Legend:

Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt



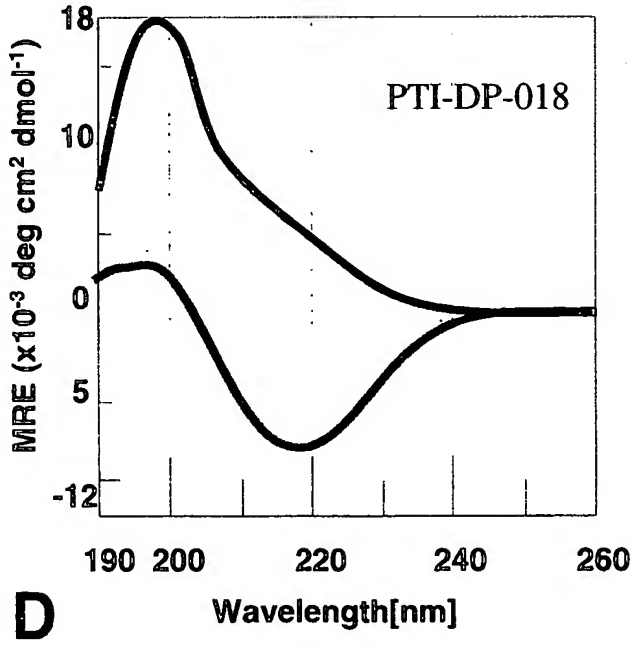
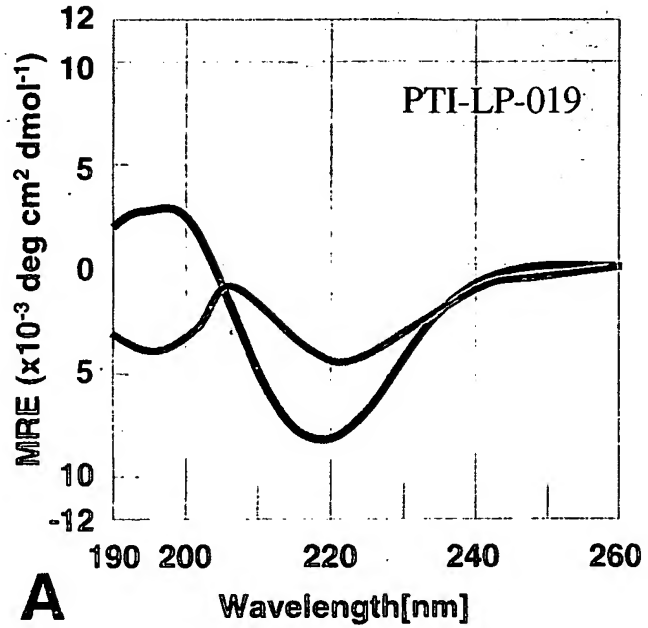
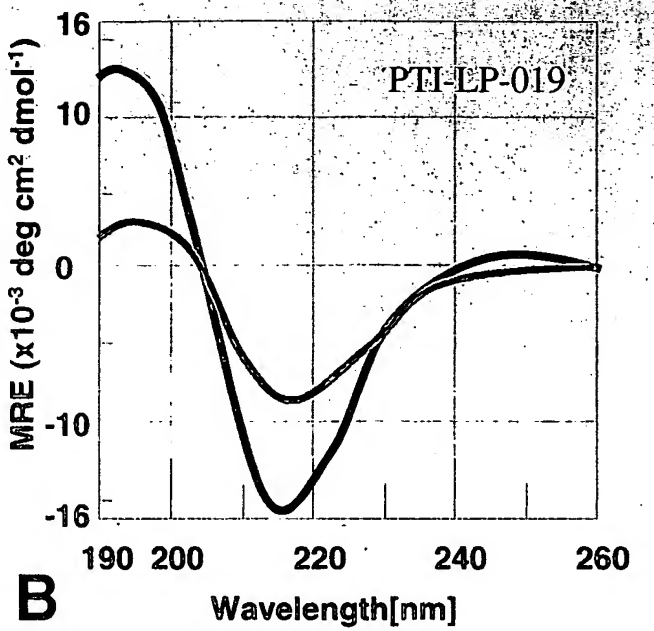


Fig. 35

CD#34



A



B

Legend:

Aβ42 Only
0.1 mg/ml

PTI-compound only
0.2 mg/ml

Aβ42 + PTI-compound
1:2 wt/wt

C

D

CD#34

Fig. 2c